GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 03:29:34 ; Search time 6787 Seconds
(without alignments)
13011.508 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 agggtcccttagccgggcgc.....tctctccccaacctcactaa 2320

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1131	48.8	1182	9	AY404343	AY404343 Homo sapi
2		754	32.5	759	7	CN396938	CN396938 170004177
3		725	31.2	879	5	BQ216829	BQ216829 AGENCOURT
4		563	24.3	916	6	CD050395	CD050395 AGENCOURT
5		457	19.7	510	7	CN396939	CN396939 170005999
6	c	430	18.5	430	1	AI917116	AI917116 ts52a02.x
7	c	422	18.2	422	1	AI580389	AI580389 tm42f08.x
8		395	17.0	481	6	CB158774	CB158774 K-EST0218

c	9	373	16.1	439	1	AA633698	AA633698 ag87a11.s
	10	345	14.9	901	4	BI827790	BI827790 603075472
c	11	328	14.1	462	5	BX109306	BX109306 BX109306
	12	305	13.1	360	5	BP431975	BP431975 BP431975
c	13	294	12.7	1055	1	AI654867	AI654867 wb65c12.x
	14	290	12.5	460	7	R19994	R19994 yg38h02.r1
c	15	286	12.3	363	2	BF510946	BF510946 UI-H-BI4-
	16	285	12.3	342	5	BP431877	BP431877 BP431877
c	17	270	11.6	357	1	AA747964	AA747964 nx79a08.s
	18	268	11.6	1180	9	AY404344	AY404344 Pan trogl
c	19	254	10.9	543	2	AW236852	AW236852 xm49h11.x
c	20	220	9.5	429	2	AW236558	AW236558 xm47g07.x
c	21	181	7.8	361	1	AA730192	AA730192 nw41a02.s
	22	181	7.8	375	1	AA715548	AA715548 nv53g11.r
	23	175	7.5	349	7	F06529	F06529 HSC1BC021 n
c	24	170	7.3	363	7	Z39483	Z39483 HSC1BC022 n
	25	167	7.2	371	2	BE843851	BE843851 RC0-TN007
c	26	105	4.5	580	8	AQ059652	AQ059652 CIT-HSP-2
	27	68	2.9	419	7	CR740722	CR740722 CR740722
c	28	68	2.9	449	1	AI217703	AI217703 qh15e09.x
c	29	68	2.9	454	1	AA970255	AA970255 op64h06.s
c	30	68	2.9	470	1	AA974327	AA974327 oq10g06.s
c	31	68	2.9	478	1	AI015041	AI015041 ov51a05.s
	32	68	2.9	552	7	CV029784	CV029784 8702 Full
c	33	68	2.9	694	2	AW173071	AW173071 xj82g11.x
	34	65	2.8	771	7	CR767782	CR767782 DKFZp469C
c	35	59	2.5	436	8	AQ476159	AQ476159 CITBI-E1-
	36	59	2.5	531	8	AQ386013	AQ386013 RPCI11-14
	37	59	2.5	751	8	AQ748070	AQ748070 HS_5538_A
c	38	55	2.4	583	1	AI694348	AI694348 wd45g04.x
	39	52	2.2	555	5	BP332215	BP332215 BP332215
c	40	47	2.0	253	1	AI373521	AI373521 qz46f08.x
c	41	47	2.0	253	1	AI492912	AI492912 qz42f01.x
c	42	47	2.0	288	2	AW235540	AW235540 xn19d12.x
c	43	47	2.0	328	1	AI671780	AI671780 wa05h05.x
c	44	47	2.0	331	1	AI613123	AI613123 ty71h04.x
c	45	47	2.0	332	1	AI672388	AI672388 ty64f01.x
c	46	47	2.0	345	2	AW779709	AW779709 hn84f05.x
c	47	47	2.0	347	1	AI767712	AI767712 wh38h05.x
	48	47	2.0	380	7	CR746104	CR746104 CR746104
	49	47	2.0	383	5	BX955526	BX955526 DKFZp781A
c	50	47	2.0	405	1	AI433413	AI433413 ti65c03.x
	51	47	2.0	459	5	BX951484	BX951484 DKFZp781F
	52	47	2.0	578	5	BP275078	BP275078 BP275078
	53	47	2.0	582	5	BP274546	BP274546 BP274546
	54	47	2.0	585	7	CR770709	CR770709 DKFZp469J
	55	47	2.0	717	7	CR769328	CR769328 DKFZp469O
	56	47	2.0	761	4	BI559553	BI559553 603252894
c	57	42	1.8	148	2	BF089587	BF089587 CM2-HT094
c	58	42	1.8	599	1	AA758115	AA758115 ah68d01.s
c	59	38	1.6	619	9	CE584093	CE584093 tigr-gss-
c	60	37	1.6	291	1	AI521956	AI521956 ti79e06.x
	61	37	1.6	565	4	BI538734	BI538734 434264 MA
c	62	37	1.6	659	6	CB435346	CB435346 615435 MA
c	63	37	1.6	706	9	CE140389	CE140389 tigr-gss-
c	64	37	1.6	799	7	CK848020	CK848020 970722 MA
c	65	35	1.5	82	1	AA974589	AA974589 op28h10.s

	66	29	1.2	209	7	CR746121	CR746121 CR746121
c	67	29	1.2	455	2	AW380602	AW380602 RC2-HT027
	68	29	1.2	1021	7	CK231266	CK231266 ILLUMIGEN
c	69	28	1.2	566	6	CB433850	CB433850 610302 MA
c	70	28	1.2	580	6	CB423692	CB423692 597208 MA
c	71	27	1.2	641	6	CD634229	CD634229 56006284H
	72	26	1.1	136	1	AA073542	AA073542 mm94b03.r
	73	26	1.1	361	1	AA730192	AA730192 nw41a02.s
c	74	26	1.1	375	1	AA715548	AA715548 nv53g11.r
	75	26	1.1	399	1	AA245658	AA245658 mx03a06.r
	76	26	1.1	428	8	AQ194654	AQ194654 RPCI11-48
	77	26	1.1	453	1	AA245657	AA245657 mx03a05.r
	78	26	1.1	473	2	BF659710	BF659710 maa23c04.
	79	26	1.1	536	2	AW226792	AW226792 um62c04.y
	80	26	1.1	538	4	BG971731	BG971731 602838268
	81	26	1.1	551	2	BF785590	BF785590 602112377
	82	26	1.1	638	4	BI103514	BI103514 602889055
	83	26	1.1	660	2	BB221592	BB221592 BB221592
	84	26	1.1	711	2	BF785562	BF785562 602112344
	85	26	1.1	713	4	BI327590	BI327590 602979770
	86	26	1.1	721	4	BG972539	BG972539 602841125
	87	26	1.1	724	6	CB952493	CB952493 AGENCOURT
	88	26	1.1	738	6	CB954127	CB954127 AGENCOURT
	89	26	1.1	758	4	BI332502	BI332502 602981312
	90	26	1.1	772	4	BI099719	BI099719 602884581
	91	26	1.1	776	2	BF781397	BF781397 602104580
	92	26	1.1	777	4	BG972946	BG972946 602840675
	93	26	1.1	782	4	BG972529	BG972529 602841114
	94	26	1.1	788	2	BF781367	BF781367 602104549
	95	26	1.1	812	4	BG969879	BG969879 602838824
	96	26	1.1	875	2	BF788790	BF788790 602107191
	97	26	1.1	880	4	BI143297	BI143297 602907843
	98	26	1.1	886	4	BI101074	BI101074 602886333
	99	26	1.1	890	4	BI101705	BI101705 602887533
	100	26	1.1	908	2	BF788011	BF788011 602113215
	101	26	1.1	910	4	BI099853	BI099853 602884666
	102	26	1.1	913	4	BG972966	BG972966 602840774
	103	26	1.1	956	2	BF784727	BF784727 602111365
	104	26	1.1	978	4	BI102968	BI102968 602888578
	105	26	1.1	1027	4	BG969791	BG969791 602838703
	106	26	1.1	1082	3	BC024453	BC024453 Mus muscu
	107	26	1.1	1185	9	AY404345	AY404345 Mus muscu
	108	26	1.1	1353	3	AK041045	AK041045 Mus muscu
	109	26	1.1	1452	2	BF782437	BF782437 602106145
	110	26	1.1	1723	3	AK052644	AK052644 Mus muscu
	111	26	1.1	2197	3	AK050128	AK050128 Mus muscu
	112	25	1.1	531	4	BI463768	BI463768 603203473
c	113	24	1.0	549	9	CE651265	CE651265 tigr-gss-
c	114	24	1.0	718	6	CD634227	CD634227 56006276H
	115	23	1.0	556	2	BF080514	BF080514 231438 MA
	116	23	1.0	899	4	BI246549	BI246549 602958449
	117	23	1.0	965	2	BF789220	BF789220 602105115
c	118	22	0.9	435	6	CB793261	CB793261 AMGNNUC:M
c	119	22	0.9	447	1	AA176547	AA176547 zp37d04.r
c	120	22	0.9	487	9	CE422925	CE422925 tigr-gss-
c	121	22	0.9	494	8	AQ185578	AQ185578 HS_2241_A
c	122	22	0.9	544	4	BG679008	BG679008 602624931

	123	22	0.9	580	9	CE054365 CE054365 tigr-gss-
	124	22	0.9	602	4	BI693709 BI693709 603342026
c	125	22	0.9	603	9	CE843398 CE843398 tigr-gss-
c	126	22	0.9	606	9	CE149561 CE149561 tigr-gss-
c	127	22	0.9	631	7	CN306203 CN306203 328823352
c	128	22	0.9	675	2	BE378177 BE378177 601237924
c	129	22	0.9	695	1	AL110426 AL110426 DKFZp434L
	130	22	0.9	751	6	CB952810 CB952810 AGENCOURT
	131	22	0.9	763	6	CD241803 CD241803 AGENCOURT
c	132	22	0.9	766	5	BU281446 BU281446 603865111
	133	22	0.9	769	9	CE543749 CE543749 tigr-gss-
c	134	22	0.9	841	2	BE378743 BE378743 601237186
c	135	22	0.9	894	4	BG747705 BG747705 602705178
c	136	21	0.9	124	8	BH104708 BH104708 RPCI-24-3
c	137	21	0.9	127	2	BF514925 BF514925 UI-H-BW1-
c	138	21	0.9	302	4	BG023045 BG023045 dab11a07.
	139	21	0.9	407	6	CB434861 CB434861 611551 MA
c	140	21	0.9	461	4	BG438773 BG438773 dab28d12.
c	141	21	0.9	485	1	AA009868 AA009868 zi07d01.r
	142	21	0.9	488	6	CB433209 CB433209 609534 MA
c	143	21	0.9	520	4	BI312811 BI312811 dai27c06.
	144	21	0.9	538	8	AQ793538 AQ793538 HS_5269_A
c	145	21	0.9	552	4	BM179355 BM179355 dai42e11.
	146	21	0.9	581	6	CA768818 CA768818 ssalbrh01
	147	21	0.9	594	5	BU664018 BU664018 cl110b07.
c	148	21	0.9	598	5	BQ400420 BQ400420 NISC_mp09
c	149	21	0.9	617	7	CN668302 CN668302 A0865D05-
	150	21	0.9	644	6	CA047596 CA047596 ssalpit15
	151	21	0.9	657	6	CA119273 CA119273 SCBGLR111
c	152	21	0.9	659	4	BI181339 BI181339 UNL-P-FN-
	153	21	0.9	691	9	CE286860 CE286860 tigr-gss-
c	154	21	0.9	718	9	CR159413 CR159413 Reverse s
c	155	21	0.9	745	6	CD634233 CD634233 56006392H
	156	21	0.9	835	9	CC577742 CC577742 CH240_456
	157	21	0.9	946	9	CL028334 CL028334 CH216-27G
	158	21	0.9	1003	9	CL021858 CL021858 CH216-8P2
	159	21	0.9	1035	9	CL112702 CL112702 ISB1-57I8
	160	21	0.9	1060	9	CL079312 CL079312 CH216-155
	161	21	0.9	1154	9	CL048289 CL048289 CH216-67L
c	162	21	0.9	1229	9	CL641750 CL641750 CH213-17F
c	163	20	0.9	169	9	CE339517 CE339517 tigr-gss-
c	164	20	0.9	194	7	H90273 H90273 yu88h02.r1
c	165	20	0.9	244	9	CE376292 CE376292 tigr-gss-
	166	20	0.9	262	9	CR037191 CR037191 Forward s
	167	20	0.9	272	9	CR504199 CR504199 Medicago
c	168	20	0.9	306	8	AZ067600 AZ067600 RPCI-23-4
	169	20	0.9	334	9	CE469814 CE469814 tigr-gss-
	170	20	0.9	357	4	BM184978 BM184978 ft84h04.y
	171	20	0.9	385	4	BI708244 BI708244 ft45a09.y
	172	20	0.9	386	4	BM534166 BM534166 fw94e12.y
	173	20	0.9	393	4	BM081091 BM081091 ft80c06.y
	174	20	0.9	394	7	CO921569 CO921569 AGENCOURT
	175	20	0.9	398	7	CO951549 CO951549 UMC-pd12f
c	176	20	0.9	409	7	CF796013 CF796013 892225 MA
c	177	20	0.9	417	9	CE656318 CE656318 tigr-gss-
	178	20	0.9	419	6	CB799389 CB799389 AMGNNUC:N
c	179	20	0.9	423	5	BY153866 BY153866 BY153866

c 180	20	0.9	434	1	AA997348	AA997348 UI-R-C0-h
181	20	0.9	434	2	BB847184	BB847184 BB847184
182	20	0.9	436	1	AV590825	AV590825 AV590825
183	20	0.9	442	4	BG145555	BG145555 uu89f10.x
184	20	0.9	443	9	CE787473	CE787473 tigr-gss-
c 185	20	0.9	450	9	AG234986	AG234986 Lotus cor
186	20	0.9	452	7	CK869895	CK869895 AGENCOURT
c 187	20	0.9	459	2	BB774032	BB774032 BB774032
188	20	0.9	459	7	CN175733	CN175733 AGENCOURT
189	20	0.9	464	8	AQ199079	AQ199079 RPCI11-67
190	20	0.9	486	9	CE410827	CE410827 tigr-gss-
191	20	0.9	535	1	AL728282	AL728282 AL728282
192	20	0.9	535	7	CK485388	CK485388 rswab0_00
193	20	0.9	537	4	BM265868	BM265868 fw36h01.y
c 194	20	0.9	537	9	CE007131	CE007131 tigr-gss-
195	20	0.9	546	9	CE154600	CE154600 tigr-gss-
196	20	0.9	552	9	CE702878	CE702878 tigr-gss-
197	20	0.9	556	8	AZ898442	AZ898442 RPCI-24-1
c 198	20	0.9	558	9	CE182816	CE182816 tigr-gss-
c 199	20	0.9	570	8	AZ719183	AZ719183 RPCI-24-1
200	20	0.9	571	9	CE062973	CE062973 tigr-gss-
201	20	0.9	572	7	CK528088	CK528088 rswfa0_00
c 202	20	0.9	575	6	CB608077	CB608077 AMGNNUC:U
c 203	20	0.9	577	5	BX372905	BX372905 BX372905
204	20	0.9	581	7	CK683510	CK683510 ZF101-P00
205	20	0.9	587	9	CE523313	CE523313 tigr-gss-
206	20	0.9	594	8	AZ519016	AZ519016 RPCI-11-6
207	20	0.9	598	7	CK543959	CK543959 rswhb0_01
c 208	20	0.9	599	1	AL728365	AL728365 AL728365
c 209	20	0.9	599	9	CC876108	CC876108 ZMMBBb019
210	20	0.9	602	9	CC519891	CC519891 CH240_367
211	20	0.9	605	9	CE712865	CE712865 tigr-gss-
212	20	0.9	606	6	CB477435	CB477435 jns21_D12
c 213	20	0.9	606	9	CE561587	CE561587 tigr-gss-
214	20	0.9	607	8	B15910	B15910 346G22.TP C
215	20	0.9	609	9	CE109632	CE109632 tigr-gss-
216	20	0.9	613	9	CE230609	CE230609 tigr-gss-
c 217	20	0.9	615	7	CF944378	CF944378 TrEST-A01
c 218	20	0.9	617	9	CE632953	CE632953 tigr-gss-
c 219	20	0.9	627	9	CE574673	CE574673 tigr-gss-
c 220	20	0.9	631	4	BG380796	BG380796 UI-R-CT0-
c 221	20	0.9	636	9	CE596340	CE596340 tigr-gss-
222	20	0.9	646	7	CF176428	CF176428 800514 MA
c 223	20	0.9	651	8	AQ422848	AQ422848 CITBI-E1-
224	20	0.9	652	7	CK490418	CK490418 rswab0_00
225	20	0.9	659	8	AZ639923	AZ639923 1M0501I11
c 226	20	0.9	660	9	CE257388	CE257388 tigr-gss-
227	20	0.9	660	9	CE708420	CE708420 tigr-gss-
228	20	0.9	661	9	CE055128	CE055128 tigr-gss-
229	20	0.9	663	9	CE360895	CE360895 tigr-gss-
c 230	20	0.9	664	9	CE576178	CE576178 tigr-gss-
c 231	20	0.9	665	2	BB624520	BB624520 BB624520
c 232	20	0.9	666	9	AG576200	AG576200 Mus muscu
233	20	0.9	672	9	CE713784	CE713784 tigr-gss-
234	20	0.9	675	9	CE378054	CE378054 tigr-gss-
235	20	0.9	679	9	AG063221	AG063221 Pan trogl
c 236	20	0.9	684	9	CE530025	CE530025 tigr-gss-

c 237	20	0.9	685	8	AZ332140	AZ332140 1M0060P17
c 238	20	0.9	692	9	CE766558	CE766558 tigr-gss-
239	20	0.9	700	1	AL714811	AL714811 AL714811
c 240	20	0.9	703	1	AL723751	AL723751 AL723751
241	20	0.9	705	1	AL718833	AL718833 AL718833
c 242	20	0.9	707	1	AL714719	AL714719 AL714719
243	20	0.9	712	9	CE701121	CE701121 tigr-gss-
c 244	20	0.9	714	9	CE210749	CE210749 tigr-gss-
245	20	0.9	731	9	CE026066	CE026066 tigr-gss-
246	20	0.9	737	9	CE324466	CE324466 tigr-gss-
c 247	20	0.9	747	8	BZ138378	BZ138378 CH230-386
c 248	20	0.9	761	9	BX993602	BX993602 Forward s
c 249	20	0.9	767	1	AL721817	AL721817 AL721817
250	20	0.9	767	9	AG532581	AG532581 Mus muscu
251	20	0.9	772	7	CV483753	CV483753 AGENCOURT
c 252	20	0.9	772	9	CE553349	CE553349 tigr-gss-
c 253	20	0.9	778	9	CG135785	CG135785 PUFNI24TD
c 254	20	0.9	781	9	AG417163	AG417163 Mus muscu
255	20	0.9	791	9	CC524962	CC524962 CH240_399
c 256	20	0.9	794	9	CR205323	CR205323 Reverse s
257	20	0.9	797	9	AJ589546	AJ589546 Arabidops
c 258	20	0.9	802	9	CE041036	CE041036 tigr-gss-
c 259	20	0.9	806	9	BX155188	BX155188 Danio rer
c 260	20	0.9	810	9	CR111618	CR111618 Reverse s
261	20	0.9	821	9	CC491351	CC491351 CH240_325
c 262	20	0.9	849	4	BJ727786	BJ727786 BJ727786
263	20	0.9	853	2	AW054025	AW054025 L30-1884T
264	20	0.9	884	8	BH130649	BH130649 ENTOW41TF
c 265	20	0.9	889	6	CA491373	CA491373 AGENCOURT
266	20	0.9	894	9	CR102774	CR102774 Forward s
c 267	20	0.9	896	9	CNS05BTS	AL330265 Tetraodon
268	20	0.9	901	9	CR270966	CR270966 Forward s
269	20	0.9	938	9	CG135784	CG135784 PUFNI24TB
270	20	0.9	942	9	CL393323	CL393323 ZMMBBb019
271	20	0.9	1036	8	CC255743	CC255743 CH261-79E
c 272	20	0.9	1062	9	CNS05BUU	AL330303 Tetraodon
c 273	20	0.9	1107	4	BM548110	BM548110 AGENCOURT
274	20	0.9	1174	8	CC203459	CC203459 CH261-47I
c 275	20	0.9	1850	3	AK033339	AK033339 Mus muscu
c 276	20	0.9	4022	3	AK041687	AK041687 Mus muscu
c 277	19	0.8	47	9	CL214736	CL214736 M073D06 G
278	19	0.8	102	8	AZ248747	AZ248747 RPCI-23-4
279	19	0.8	104	2	AW709225	AW709225 d3g08ne.f
280	19	0.8	122	4	BG952052	BG952052 MR1-CT073
c 281	19	0.8	124	4	BG950878	BG950878 MR1-CT073
282	19	0.8	147	9	LBAF004H05	BX539790 Leishmani
c 283	19	0.8	159	8	AZ633044	AZ633044 1M0488I04
284	19	0.8	160	7	CO356090	CO356090 DR_ATE_NR
c 285	19	0.8	171	9	CE433379	CE433379 tigr-gss-
286	19	0.8	180	9	CE204377	CE204377 tigr-gss-
c 287	19	0.8	182	2	BE149929	BE149929 RC0-HT025
c 288	19	0.8	199	9	CE588538	CE588538 tigr-gss-
289	19	0.8	207	9	CE738101	CE738101 tigr-gss-
c 290	19	0.8	209	9	CNS02ECX	AL193578 Tetraodon
291	19	0.8	210	1	AJ282887	AJ282887 4A3A-P10F
292	19	0.8	211	2	BE149928	BE149928 RC0-HT025
c 293	19	0.8	213	9	CE067769	CE067769 tigr-gss-

294	19	0.8	214	2	AW815495	AW815495 QV0-ST021
c 295	19	0.8	214	9	CE208799	CE208799 tigr-gss-
296	19	0.8	214	9	CE726333	CE726333 tigr-gss-
c 297	19	0.8	215	9	CE414518	CE414518 tigr-gss-
298	19	0.8	224	9	CE520482	CE520482 tigr-gss-
c 299	19	0.8	227	9	BX534851	BX534851 Arabidops
300	19	0.8	229	8	BH655130	BH655130 BOHXI15TF
c 301	19	0.8	231	9	CE760820	CE760820 tigr-gss-
c 302	19	0.8	235	9	CE200414	CE200414 tigr-gss-
c 303	19	0.8	236	9	CE077168	CE077168 tigr-gss-
c 304	19	0.8	236	9	CE327796	CE327796 tigr-gss-
c 305	19	0.8	237	9	CE072544	CE072544 tigr-gss-
c 306	19	0.8	238	2	BB262215	BB262215 BB262215
c 307	19	0.8	239	5	BU386241	BU386241 603860930
c 308	19	0.8	242	9	CE539955	CE539955 tigr-gss-
309	19	0.8	249	9	CE030499	CE030499 tigr-gss-
c 310	19	0.8	250	9	CE486471	CE486471 tigr-gss-
311	19	0.8	251	9	CL449822	CL449822 ZMMBBb047
312	19	0.8	252	9	CL959889	CL959889 OsIFCC036
313	19	0.8	257	7	CK614293	CK614293 LPSe_D23
314	19	0.8	259	9	CE627861	CE627861 tigr-gss-
315	19	0.8	260	1	AV274662	AV274662 AV274662
c 316	19	0.8	262	7	F04518	F04518 HSCZPH012 n
c 317	19	0.8	263	1	AI094659	AI094659 oy61f01.s
c 318	19	0.8	264	1	AA296900	AA296900 EST112458
319	19	0.8	265	6	CA950542	CA950542 ir90c01.y
c 320	19	0.8	268	2	BB466444	BB466444 BB466444
321	19	0.8	269	9	CE018071	CE018071 tigr-gss-
322	19	0.8	269	9	CE512239	CE512239 tigr-gss-
c 323	19	0.8	271	2	BB528131	BB528131 BB528131
c 324	19	0.8	272	9	CE324366	CE324366 tigr-gss-
325	19	0.8	274	9	CE538693	CE538693 tigr-gss-
c 326	19	0.8	277	1	AV217821	AV217821 AV217821
327	19	0.8	277	9	CE266163	CE266163 tigr-gss-
c 328	19	0.8	280	9	CE653527	CE653527 tigr-gss-
329	19	0.8	284	9	CE710156	CE710156 tigr-gss-
c 330	19	0.8	285	6	CF032947	CF032947 QCF10c12.
c 331	19	0.8	285	9	CE632956	CE632956 tigr-gss-
c 332	19	0.8	286	9	CE484767	CE484767 tigr-gss-
c 333	19	0.8	287	2	BB191017	BB191017 BB191017
c 334	19	0.8	287	9	CE539872	CE539872 tigr-gss-
c 335	19	0.8	289	2	BB267346	BB267346 BB267346
c 336	19	0.8	289	6	CD152000	CD152000 ML1-0027T
c 337	19	0.8	291	9	CE182081	CE182081 tigr-gss-
338	19	0.8	292	9	CE028288	CE028288 tigr-gss-
c 339	19	0.8	293	2	BB264514	BB264514 BB264514
c 340	19	0.8	294	7	CN351899	CN351899 170005328
c 341	19	0.8	294	9	CE543781	CE543781 tigr-gss-
c 342	19	0.8	296	6	CD612735	CD612735 56029315J
343	19	0.8	297	9	CE420939	CE420939 tigr-gss-
344	19	0.8	298	9	CG914090	CG914090 ZMMBBb037
345	19	0.8	299	2	AW713801	AW713801 h2g11ne.f
346	19	0.8	299	6	CD612734	CD612734 56029315H
c 347	19	0.8	300	9	BX004009	BX004009 Arabidops
348	19	0.8	304	9	CE575398	CE575398 tigr-gss-
c 349	19	0.8	307	1	AI435198	AI435198 ti11a01.x
c 350	19	0.8	307	9	CE454878	CE454878 tigr-gss-

351	19	0.8	307	9	CE483853	CE483853 tigr-gss-
352	19	0.8	309	9	CE370950	CE370950 tigr-gss-
c 353	19	0.8	310	2	BB103174	BB103174 BB103174
354	19	0.8	315	9	CE164303	CE164303 tigr-gss-
c 355	19	0.8	315	9	CE570748	CE570748 tigr-gss-
c 356	19	0.8	316	9	CE106984	CE106984 tigr-gss-
357	19	0.8	316	9	CE408328	CE408328 tigr-gss-
c 358	19	0.8	316	9	CE732166	CE732166 tigr-gss-
c 359	19	0.8	317	9	BX660820	BX660820 Arabidops
360	19	0.8	318	4	BI800097	BI800097 H147F08 E
c 361	19	0.8	319	7	T24109	T24109 seq2297 Cot
c 362	19	0.8	321	8	AZ564000	AZ564000 RPCI-23-2
c 363	19	0.8	321	9	CE016313	CE016313 tigr-gss-
c 364	19	0.8	323	1	AV683895	AV683895 AV683895
c 365	19	0.8	323	9	CE204559	CE204559 tigr-gss-
c 366	19	0.8	324	1	AI886619	AI886619 tz59h04.x
367	19	0.8	324	9	CL980220	CL980220 OsIFCC034
368	19	0.8	325	6	CD959714	CD959714 SCY_111 G
c 369	19	0.8	326	5	BY110280	BY110280 BY110280
370	19	0.8	326	7	CV165679	CV165679 rsmsxl_00
371	19	0.8	326	9	CE308758	CE308758 tigr-gss-
c 372	19	0.8	327	5	BY107492	BY107492 BY107492
c 373	19	0.8	329	2	BE711259	BE711259 RC6-HT067
c 374	19	0.8	329	5	BY110750	BY110750 BY110750
c 375	19	0.8	331	9	CE523580	CE523580 tigr-gss-
376	19	0.8	335	9	CE033215	CE033215 tigr-gss-
377	19	0.8	338	9	CE564098	CE564098 tigr-gss-
378	19	0.8	339	9	CE591396	CE591396 tigr-gss-
379	19	0.8	340	5	BU853917	BU853917 AGENCOURT
c 380	19	0.8	342	9	CE238041	CE238041 tigr-gss-
381	19	0.8	343	2	AW480786	AW480786 33285 MAR
c 382	19	0.8	347	9	CE796067	CE796067 tigr-gss-
383	19	0.8	350	9	CE096783	CE096783 tigr-gss-
384	19	0.8	357	9	CE443622	CE443622 tigr-gss-
c 385	19	0.8	358	9	CE582615	CE582615 tigr-gss-
c 386	19	0.8	359	1	AI522340	AI522340 fb18e12.x
387	19	0.8	359	2	BE415737	BE415737 MWL039.B0
388	19	0.8	359	9	CE351850	CE351850 tigr-gss-
389	19	0.8	360	9	CE732059	CE732059 tigr-gss-
c 390	19	0.8	362	8	BZ133937	BZ133937 CH230-385
c 391	19	0.8	363	9	CE163338	CE163338 tigr-gss-
c 392	19	0.8	364	7	CK764274	CK764274 pam01-13m
393	19	0.8	364	9	CE690486	CE690486 tigr-gss-
394	19	0.8	366	9	CE172310	CE172310 tigr-gss-
395	19	0.8	368	9	CE805087	CE805087 tigr-gss-
c 396	19	0.8	370	9	CE216693	CE216693 tigr-gss-
c 397	19	0.8	371	2	AW674454	AW674454 ba63c01.x
c 398	19	0.8	371	9	CE125478	CE125478 tigr-gss-
399	19	0.8	372	9	CE429239	CE429239 tigr-gss-
400	19	0.8	373	9	CE723064	CE723064 tigr-gss-
401	19	0.8	374	9	CE041628	CE041628 tigr-gss-
402	19	0.8	374	9	CE524318	CE524318 tigr-gss-
c 403	19	0.8	376	1	AI734930	AI734930 at14d05.x
c 404	19	0.8	376	7	CF230525	CF230525 PtaC0009D
405	19	0.8	377	9	CE694673	CE694673 tigr-gss-
c 406	19	0.8	380	9	CE308274	CE308274 tigr-gss-
c 407	19	0.8	381	9	CE658419	CE658419 tigr-gss-

408	19	0.8	382	9	CE466702	CE466702 tigr-gss-
c 409	19	0.8	382	9	CE487403	CE487403 tigr-gss-
410	19	0.8	383	4	BI131705	BI131705 G124P56Y
411	19	0.8	383	5	BY006002	BY006002 BY006002
412	19	0.8	384	8	AQ807226	AQ807226 HS_3127_B
c 413	19	0.8	384	8	AQ580886	AQ580886 RPCI-11-4
c 414	19	0.8	386	9	CE743865	CE743865 tigr-gss-
415	19	0.8	388	2	AW434729	AW434729 UI-R-BJ0p
416	19	0.8	389	1	AA397322	AA397322 mr40b11.r
c 417	19	0.8	390	9	CE194014	CE194014 tigr-gss-
c 418	19	0.8	391	5	BP650827	BP650827 BP650827
c 419	19	0.8	391	9	CE263871	CE263871 tigr-gss-
c 420	19	0.8	392	6	CB774799	CB774799 AMGNNUC:S
421	19	0.8	393	9	CE159307	CE159307 tigr-gss-
422	19	0.8	393	9	CE275945	CE275945 tigr-gss-
c 423	19	0.8	395	9	CE388438	CE388438 tigr-gss-
c 424	19	0.8	396	4	BG883353	BG883353 fp26f01.x
c 425	19	0.8	396	7	CF231111	CF231111 PtaC0017E
c 426	19	0.8	397	9	CE171641	CE171641 tigr-gss-
c 427	19	0.8	398	8	AQ145732	AQ145732 HS_2216_A
428	19	0.8	399	9	CE440871	CE440871 tigr-gss-
429	19	0.8	400	9	CE310652	CE310652 tigr-gss-
430	19	0.8	402	9	CE248134	CE248134 tigr-gss-
431	19	0.8	402	9	CE596949	CE596949 tigr-gss-
c 432	19	0.8	404	9	CC795797	CC795797 SALK_0883
433	19	0.8	405	6	CD407923	CD407923 Gm_ck3369
434	19	0.8	407	9	CE280199	CE280199 tigr-gss-
c 435	19	0.8	410	2	BE172984	BE172984 MR0-HT055
c 436	19	0.8	410	7	R14675	R14675 yf92b05.r1
c 437	19	0.8	410	9	CE785393	CE785393 tigr-gss-
438	19	0.8	412	9	AL768945	AL768945 Arabidops
439	19	0.8	412	9	CC958229	CC958229 BOICX65TR
c 440	19	0.8	413	4	BI129781	BI129781 G095P54Y
c 441	19	0.8	413	8	AQ435710	AQ435710 HS_5148_B
442	19	0.8	415	6	CB800643	CB800643 AMGNNUC:S
443	19	0.8	416	5	BY246714	BY246714 BY246714
c 444	19	0.8	416	9	CE762505	CE762505 tigr-gss-
445	19	0.8	419	8	BZ913278	BZ913278 CH240_53P
446	19	0.8	421	2	BB704505	BB704505 BB704505
447	19	0.8	421	8	BZ384590	BZ384590 SALK_1357
c 448	19	0.8	422	9	CE742419	CE742419 tigr-gss-
c 449	19	0.8	424	8	BZ415985	BZ415985 if61h03.g
c 450	19	0.8	426	8	AZ151834	AZ151834 SP_0038_B
c 451	19	0.8	427	9	CE053127	CE053127 tigr-gss-
452	19	0.8	427	9	CE651624	CE651624 tigr-gss-
c 453	19	0.8	428	7	N24605	N24605 yx72e05.s1
454	19	0.8	429	1	AA797863	AA797863 vw31g10.r
455	19	0.8	429	5	BY180909	BY180909 BY180909
456	19	0.8	429	8	BZ943150	BZ943150 CH240_80H
457	19	0.8	429	8	AQ636784	AQ636784 RPCI-11-4
c 458	19	0.8	429	9	CE054838	CE054838 tigr-gss-
459	19	0.8	431	9	CE022381	CE022381 tigr-gss-
c 460	19	0.8	431	9	CE168437	CE168437 tigr-gss-
c 461	19	0.8	431	9	CE401510	CE401510 tigr-gss-
c 462	19	0.8	431	9	CG398567	CG398567 ZMMBBc001
463	19	0.8	433	5	BY283433	BY283433 BY283433
c 464	19	0.8	434	9	AG195209	AG195209 Pan trogl

c 465	19	0.8	435	6	BY532671	BY532671 BY532671
c 466	19	0.8	435	6	CA799585	CA799585 sat35h11.
c 467	19	0.8	435	8	BH749116	BH749116 SALK_0473
c 468	19	0.8	435	9	CE418826	CE418826 tigr-gss-
469	19	0.8	435	9	CE632990	CE632990 tigr-gss-
c 470	19	0.8	436	2	AW228656	AW228656 up15h09.x
c 471	19	0.8	436	2	BE350286	BE350286 ht12f08.x
c 472	19	0.8	436	4	BI293355	BI293355 UI-R-DK0-
c 473	19	0.8	436	9	CE812891	CE812891 tigr-gss-
474	19	0.8	438	9	CE246842	CE246842 tigr-gss-
c 475	19	0.8	439	7	CN399825	CN399825 170004243
476	19	0.8	439	9	CE532786	CE532786 tigr-gss-
c 477	19	0.8	442	7	CN967657	CN967657 15154_100
478	19	0.8	442	9	CE082046	CE082046 tigr-gss-
c 479	19	0.8	442	9	CE643112	CE643112 tigr-gss-
c 480	19	0.8	444	1	AV723736	AV723736 AV723736
c 481	19	0.8	446	8	AQ154983	AQ154983 HS_3037_A
482	19	0.8	448	9	CE783536	CE783536 tigr-gss-
483	19	0.8	449	1	AL828300	AL828300 AL828300
c 484	19	0.8	449	6	CD555738	CD555738 B0397B11-
c 485	19	0.8	449	9	CE675203	CE675203 tigr-gss-
486	19	0.8	450	8	AQ027077	AQ027077 CIT-HSP-2
c 487	19	0.8	450	9	CE699613	CE699613 tigr-gss-
c 488	19	0.8	451	9	CE084498	CE084498 tigr-gss-
c 489	19	0.8	452	2	BF887837	BF887837 QV2-TN017
490	19	0.8	452	2	BB839850	BB839850 BB839850
c 491	19	0.8	452	2	BE335337	BE335337 ug98d07.x
492	19	0.8	452	6	CD159837	CD159837 ML1-0064P
c 493	19	0.8	452	9	CE678493	CE678493 tigr-gss-
c 494	19	0.8	453	8	AZ419750	AZ419750 1M0196I13
495	19	0.8	453	8	AQ208915	AQ208915 HS_3230_A
496	19	0.8	454	5	BY252260	BY252260 BY252260
497	19	0.8	454	9	CE242539	CE242539 tigr-gss-
c 498	19	0.8	455	2	BF711381	BF711381 MI-P-A1-a
499	19	0.8	455	5	BY239481	BY239481 BY239481
500	19	0.8	456	4	BG012069	BG012069 RC3-GN027
c 501	19	0.8	457	2	BF706341	BF706341 280656 MA
502	19	0.8	457	4	BI060835	BI060835 IL3-UT011
c 503	19	0.8	457	9	CE316095	CE316095 tigr-gss-
504	19	0.8	458	4	BI060832	BI060832 IL3-UT011
505	19	0.8	458	7	N62141	N62141 yz62b07.s1
c 506	19	0.8	459	8	BH327848	BH327848 CH230-45O
507	19	0.8	461	9	CE659288	CE659288 tigr-gss-
c 508	19	0.8	462	8	BZ198526	BZ198526 CH230-322
509	19	0.8	463	9	CE208987	CE208987 tigr-gss-
c 510	19	0.8	463	9	CE415203	CE415203 tigr-gss-
511	19	0.8	463	9	CE622682	CE622682 tigr-gss-
512	19	0.8	465	2	AW710350	AW710350 e3b03ne.f
c 513	19	0.8	466	8	AZ419439	AZ419439 1M0195O23
c 514	19	0.8	467	8	CC168193	CC168193 ij83a08.b
515	19	0.8	468	6	CD740207	CD740207 4029011 1
516	19	0.8	468	8	AZ845709	AZ845709 2M0145D12
c 517	19	0.8	468	8	BZ187606	BZ187606 CH230-435
518	19	0.8	469	6	CD878973	CD878973 AZO4.104A
c 519	19	0.8	469	7	H44410	H44410 yo74d04.s1
520	19	0.8	470	2	BE848382	BE848382 uw37h11.y
c 521	19	0.8	470	9	CE398868	CE398868 tigr-gss-

c 522	19	0.8	470	9	CE403345	CE403345 tigr-gss-
c 523	19	0.8	471	9	CE701710	CE701710 tigr-gss-
524	19	0.8	472	4	BG148767	BG148767 uu81a02.y
c 525	19	0.8	472	9	CE717772	CE717772 tigr-gss-
526	19	0.8	473	6	CD160420	CD160420 ML1-0066G
527	19	0.8	473	8	BH030764	BH030764 RPCI-24-2
c 528	19	0.8	473	9	CE601638	CE601638 tigr-gss-
529	19	0.8	475	8	AQ616676	AQ616676 HS_5153_A
530	19	0.8	476	4	BG383826	BG383826 302221 MA
531	19	0.8	476	9	CE279300	CE279300 tigr-gss-
532	19	0.8	477	8	AZ889580	AZ889580 RPCI-24-1
533	19	0.8	479	9	CE013496	CE013496 tigr-gss-
c 534	19	0.8	481	8	BZ311544	BZ311544 ic69c07.b
535	19	0.8	481	9	CE053817	CE053817 tigr-gss-
536	19	0.8	482	9	CE653044	CE653044 tigr-gss-
537	19	0.8	482	9	CE769211	CE769211 tigr-gss-
c 538	19	0.8	483	6	CD297498	CD297498 StrPu691.
c 539	19	0.8	483	7	CK555864	CK555864 rswla0_02
540	19	0.8	484	9	CE408225	CE408225 tigr-gss-
541	19	0.8	485	8	BH776532	BH776532 fzmb013f0
542	19	0.8	486	9	CE122510	CE122510 tigr-gss-
c 543	19	0.8	486	9	CE613461	CE613461 tigr-gss-
c 544	19	0.8	487	7	CN679395	CN679395 E0123H09-
c 545	19	0.8	487	8	BZ159296	BZ159296 CH230-289
546	19	0.8	488	6	CA656546	CA656546 wlm0.pk00
547	19	0.8	488	7	CN792544	CN792544 4127418 B
548	19	0.8	491	9	CE110968	CE110968 tigr-gss-
549	19	0.8	491	9	CE347474	CE347474 tigr-gss-
550	19	0.8	493	8	AZ891386	AZ891386 RPCI-24-1
551	19	0.8	493	9	CE060627	CE060627 tigr-gss-
552	19	0.8	493	9	CE717097	CE717097 tigr-gss-
553	19	0.8	494	9	CE649507	CE649507 tigr-gss-
c 554	19	0.8	495	9	CE265505	CE265505 tigr-gss-
555	19	0.8	496	9	CE087107	CE087107 tigr-gss-
c 556	19	0.8	496	9	CE374119	CE374119 tigr-gss-
c 557	19	0.8	496	9	CE806116	CE806116 tigr-gss-
c 558	19	0.8	497	5	BU738882	BU738882 UI-E-EJ0-
559	19	0.8	497	9	CE012709	CE012709 tigr-gss-
560	19	0.8	497	9	CE068561	CE068561 tigr-gss-
561	19	0.8	498	7	CK738707	CK738707 OF04F03-T
c 562	19	0.8	498	9	CE094979	CE094979 tigr-gss-
c 563	19	0.8	501	9	CE188918	CE188918 tigr-gss-
564	19	0.8	501	9	CE750586	CE750586 tigr-gss-
565	19	0.8	502	5	BX921161	BX921161 BX921161
566	19	0.8	502	6	CD150391	CD150391 ML1-0020T
c 567	19	0.8	502	7	R43640	R43640 yg20g08.s1
c 568	19	0.8	502	9	CE619628	CE619628 tigr-gss-
c 569	19	0.8	502	9	CE640383	CE640383 tigr-gss-
570	19	0.8	503	9	CE331433	CE331433 tigr-gss-
571	19	0.8	503	9	CE413671	CE413671 tigr-gss-
572	19	0.8	504	9	CE588004	CE588004 tigr-gss-
573	19	0.8	505	2	BE040658	BE040658 OF04F03 O
574	19	0.8	505	4	BG467088	BG467088 1A04D04 B
575	19	0.8	505	9	CE505312	CE505312 tigr-gss-
576	19	0.8	505	9	CE787301	CE787301 tigr-gss-
c 577	19	0.8	506	6	CD096095	CD096095 ME1-0006T
578	19	0.8	506	7	CV162940	CV162940 rsmsxl_00

c	579	19	0.8	506	9	CE729747 CE729747 tigr-gss-
	580	19	0.8	507	9	CE292269 CE292269 tigr-gss-
	581	19	0.8	510	4	BG263863 BG263863 WHE2338_H
c	582	19	0.8	510	8	AQ625249 AQ625249 CITBI-E1-
c	583	19	0.8	510	9	CE476530 CE476530 tigr-gss-
	584	19	0.8	512	5	BY248575 BY248575 BY248575
c	585	19	0.8	512	7	R59128 R59128 yg96b12.s1
	586	19	0.8	512	9	CE279895 CE279895 tigr-gss-
	587	19	0.8	514	4	BI127207 BI127207 G004P63Y
	588	19	0.8	514	9	CE549647 CE549647 tigr-gss-
	589	19	0.8	514	9	CE552711 CE552711 tigr-gss-
	590	19	0.8	514	9	CE839568 CE839568 tigr-gss-
c	591	19	0.8	515	6	CB164148 CB164148 K-EST0225
c	592	19	0.8	515	8	BZ723789 BZ723789 PUCFG90TD
	593	19	0.8	515	9	CE538885 CE538885 tigr-gss-
	594	19	0.8	517	6	CA546327 CA546327 K0129E03-
c	595	19	0.8	518	5	BX102827 BX102827 BX102827
	596	19	0.8	518	6	CA662859 CA662859 wlmk1.pk0
c	597	19	0.8	521	6	CB482157 CB482157 jns87_G12
c	598	19	0.8	521	9	CE733391 CE733391 tigr-gss-
	599	19	0.8	522	9	CC943643 CC943643 BOICC06TR
	600	19	0.8	522	9	CE059764 CE059764 tigr-gss-
	601	19	0.8	524	2	BE429494 BE429494 TAS000.G0
c	602	19	0.8	525	8	AQ388687 AQ388687 RPCI11-15
c	603	19	0.8	525	9	CE403020 CE403020 tigr-gss-
	604	19	0.8	527	9	CE490696 CE490696 tigr-gss-
c	605	19	0.8	527	9	CE613173 CE613173 tigr-gss-
c	606	19	0.8	528	9	CE482497 CE482497 tigr-gss-
	607	19	0.8	529	6	CB555240 CB555240 MMSP0079_
	608	19	0.8	529	9	CE487945 CE487945 tigr-gss-
	609	19	0.8	530	4	BG226743 BG226743 kp93a04.y
	610	19	0.8	530	9	CE541514 CE541514 tigr-gss-
	611	19	0.8	531	7	CK680830 CK680830 ZF101-P00
	612	19	0.8	531	9	CE219792 CE219792 tigr-gss-
	613	19	0.8	531	9	CE717244 CE717244 tigr-gss-
c	614	19	0.8	532	9	CE007968 CE007968 tigr-gss-
c	615	19	0.8	532	9	CE597285 CE597285 tigr-gss-
	616	19	0.8	532	9	CE626023 CE626023 tigr-gss-
	617	19	0.8	534	7	CF303787 CF303787 ABF1--03-
	618	19	0.8	536	9	CE124294 CE124294 tigr-gss-
c	619	19	0.8	537	9	CE463095 CE463095 tigr-gss-
c	620	19	0.8	537	9	CE633358 CE633358 tigr-gss-
	621	19	0.8	538	9	CE247788 CE247788 tigr-gss-
	622	19	0.8	539	2	AW239732 AW239732 pti1c.pk0
	623	19	0.8	539	9	CE175029 CE175029 tigr-gss-
c	624	19	0.8	540	2	AW189966 AW189966 xl10g04.x
	625	19	0.8	541	2	BE031534 BE031534 130138 MA
	626	19	0.8	541	7	CN231669 CN231669 WLB043E11
	627	19	0.8	542	8	AZ274374 AZ274374 RPCI-23-1
c	628	19	0.8	542	9	CL372046 CL372046 RPCI44_30
	629	19	0.8	543	5	BP165805 BP165805 BP165805
c	630	19	0.8	543	6	CD095982 CD095982 ME1-0006T
	631	19	0.8	544	9	CE509611 CE509611 tigr-gss-
c	632	19	0.8	544	9	CE527528 CE527528 tigr-gss-
	633	19	0.8	545	9	CE297785 CE297785 tigr-gss-
	634	19	0.8	546	4	BF991122 BF991122 MR1-GN017
	635	19	0.8	547	7	CK332163 CK332163 H8192C04-

636	19	0.8	547	9	CE161422	CE161422 tigr-gss-
637	19	0.8	547	9	CE172064	CE172064 tigr-gss-
c 638	19	0.8	547	9	CE331107	CE331107 tigr-gss-
c 639	19	0.8	548	9	CE030234	CE030234 tigr-gss-
640	19	0.8	548	9	CE553198	CE553198 tigr-gss-
641	19	0.8	548	9	CE575934	CE575934 tigr-gss-
c 642	19	0.8	548	9	CE715396	CE715396 tigr-gss-
643	19	0.8	549	6	CF039804	CF039804 QCH4e10.y
c 644	19	0.8	549	9	CE036126	CE036126 tigr-gss-
c 645	19	0.8	550	9	CE099811	CE099811 tigr-gss-
c 646	19	0.8	551	9	CE412962	CE412962 tigr-gss-
647	19	0.8	551	9	CE448884	CE448884 tigr-gss-
648	19	0.8	552	9	CE313032	CE313032 tigr-gss-
649	19	0.8	552	9	CE346760	CE346760 tigr-gss-
c 650	19	0.8	552	9	CE706206	CE706206 tigr-gss-
651	19	0.8	553	9	BX239149	BX239149 Danio rer
652	19	0.8	553	9	CE631870	CE631870 tigr-gss-
c 653	19	0.8	554	9	CL414099	CL414099 RPCI44_43
c 654	19	0.8	555	2	AW975322	AW975322 EST387430
c 655	19	0.8	555	4	BG352898	BG352898 sab92g05.
656	19	0.8	555	9	CE123576	CE123576 tigr-gss-
657	19	0.8	556	9	CE037936	CE037936 tigr-gss-
658	19	0.8	556	9	CE462431	CE462431 tigr-gss-
659	19	0.8	556	9	CE657014	CE657014 tigr-gss-
660	19	0.8	557	9	CE812347	CE812347 tigr-gss-
661	19	0.8	558	9	CE112077	CE112077 tigr-gss-
662	19	0.8	558	9	CE113282	CE113282 tigr-gss-
c 663	19	0.8	558	9	CE259404	CE259404 tigr-gss-
664	19	0.8	558	9	CE555033	CE555033 tigr-gss-
665	19	0.8	558	9	CE627220	CE627220 tigr-gss-
666	19	0.8	559	7	CN291419	CN291419 170006000
667	19	0.8	559	9	CE575016	CE575016 tigr-gss-
668	19	0.8	559	9	CE718853	CE718853 tigr-gss-
c 669	19	0.8	560	7	CF230998	CF230998 PtaC0016B
670	19	0.8	560	8	BZ718661	BZ718661 PUCFF22TD
671	19	0.8	560	9	CE561295	CE561295 tigr-gss-
c 672	19	0.8	561	5	BX351016	BX351016 BX351016
c 673	19	0.8	562	9	CE498349	CE498349 tigr-gss-
674	19	0.8	562	9	CE561160	CE561160 tigr-gss-
c 675	19	0.8	563	8	AQ510431	AQ510431 nbxb0095M
676	19	0.8	563	9	CE371029	CE371029 tigr-gss-
c 677	19	0.8	564	9	CE040030	CE040030 tigr-gss-
c 678	19	0.8	565	5	BU610740	BU610740 UI-M-FC0-
c 679	19	0.8	565	6	CD095805	CD095805 ME1-0006T
c 680	19	0.8	565	8	AZ601443	AZ601443 1M0419P09
681	19	0.8	565	9	CE684214	CE684214 tigr-gss-
682	19	0.8	566	8	BH327339	BH327339 CH230-105
683	19	0.8	566	9	CE043674	CE043674 tigr-gss-
c 684	19	0.8	568	9	CE043736	CE043736 tigr-gss-
685	19	0.8	568	9	CE143254	CE143254 tigr-gss-
c 686	19	0.8	568	9	CE649747	CE649747 tigr-gss-
687	19	0.8	568	9	CE812360	CE812360 tigr-gss-
c 688	19	0.8	569	9	CE352673	CE352673 tigr-gss-
689	19	0.8	569	9	CE543510	CE543510 tigr-gss-
690	19	0.8	569	9	CE636208	CE636208 tigr-gss-
c 691	19	0.8	570	7	CF611501	CF611501 Lr_Cd2CF_
c 692	19	0.8	571	7	CF571043	CF571043 MCS008H09

	693	19	0.8	571	9	CE816035	CE816035 tigr-gss-
	694	19	0.8	572	6	CA733078	CA733078 wlp1c.pk0
	695	19	0.8	572	9	CE359182	CE359182 tigr-gss-
	696	19	0.8	573	9	CE206234	CE206234 tigr-gss-
c	697	19	0.8	573	9	CE257376	CE257376 tigr-gss-
c	698	19	0.8	573	9	CE444590	CE444590 tigr-gss-
	699	19	0.8	576	9	CE242973	CE242973 tigr-gss-
	700	19	0.8	577	9	CE313890	CE313890 tigr-gss-
	701	19	0.8	577	9	CE408304	CE408304 tigr-gss-
	702	19	0.8	577	9	CE600265	CE600265 tigr-gss-
c	703	19	0.8	577	9	CE620115	CE620115 tigr-gss-
	704	19	0.8	578	6	CA929693	CA929693 MTU2CA.P1
	705	19	0.8	578	9	CE324758	CE324758 tigr-gss-
	706	19	0.8	579	9	CE096313	CE096313 tigr-gss-
	707	19	0.8	580	9	CE283406	CE283406 tigr-gss-
	708	19	0.8	580	9	CE391770	CE391770 tigr-gss-
c	709	19	0.8	580	9	CE694128	CE694128 tigr-gss-
c	710	19	0.8	581	6	CB586906	CB586906 AMGNNUC:N
c	711	19	0.8	582	5	BQ537054	BQ537054 STEM2_19_
c	712	19	0.8	582	9	CE291831	CE291831 tigr-gss-
c	713	19	0.8	582	9	CE653526	CE653526 tigr-gss-
c	714	19	0.8	582	9	CE823136	CE823136 tigr-gss-
c	715	19	0.8	583	9	CE677489	CE677489 tigr-gss-
	716	19	0.8	583	9	CE787283	CE787283 tigr-gss-
	717	19	0.8	583	9	CE853194	CE853194 tigr-gss-
c	718	19	0.8	584	8	AZ352712	AZ352712 1M0091K16
	719	19	0.8	584	9	CE064780	CE064780 tigr-gss-
	720	19	0.8	584	9	CE367487	CE367487 tigr-gss-
	721	19	0.8	585	7	CF354804	CF354804 lac18e03.
c	722	19	0.8	585	8	BZ516376	BZ516376 BOMQT40TF
	723	19	0.8	585	9	CE086408	CE086408 tigr-gss-
	724	19	0.8	585	9	CE105967	CE105967 tigr-gss-
c	725	19	0.8	585	9	CE196653	CE196653 tigr-gss-
c	726	19	0.8	586	9	CE146890	CE146890 tigr-gss-
	727	19	0.8	586	9	CE411571	CE411571 tigr-gss-
c	728	19	0.8	587	1	AJ658082	AJ658082 AJ658082
	729	19	0.8	588	5	BU372677	BU372677 603590261
c	730	19	0.8	588	9	CE529559	CE529559 tigr-gss-
	731	19	0.8	589	5	BQ116446	BQ116446 EST602022
	732	19	0.8	589	9	CE113227	CE113227 tigr-gss-
c	733	19	0.8	589	9	CE524897	CE524897 tigr-gss-
	734	19	0.8	590	7	CF111951	CF111951 Shultzomi
	735	19	0.8	591	9	CE193352	CE193352 tigr-gss-
c	736	19	0.8	592	9	CE291854	CE291854 tigr-gss-
	737	19	0.8	592	9	CE478157	CE478157 tigr-gss-
	738	19	0.8	593	5	BQ553158	BQ553158 H4020D04-
	739	19	0.8	593	9	CR478931	CR478931 Medicago
	740	19	0.8	594	9	CE013914	CE013914 tigr-gss-
c	741	19	0.8	594	9	CE203000	CE203000 tigr-gss-
c	742	19	0.8	596	4	BI710340	BI710340 fq35a02.x
c	743	19	0.8	596	5	BX502501	BX502501 DKFZp779G
c	744	19	0.8	596	8	AQ637709	AQ637709 RPCI-11-4
c	745	19	0.8	596	9	CE116099	CE116099 tigr-gss-
	746	19	0.8	596	9	CE298935	CE298935 tigr-gss-
	747	19	0.8	596	9	CE379735	CE379735 tigr-gss-
	748	19	0.8	596	9	CE653623	CE653623 tigr-gss-
	749	19	0.8	596	9	CE827628	CE827628 tigr-gss-

	750	19	0.8	597	1	AL725528	AL725528 AL725528
	751	19	0.8	597	6	CB455366	CB455366 712504 MA
	752	19	0.8	597	9	CE222134	CE222134 tigr-gss-
	753	19	0.8	598	6	CA726716	CA726716 wde1f.pk0
	754	19	0.8	598	6	CD217981	CD217981 pgr1n.pk0
	755	19	0.8	598	9	CE334679	CE334679 tigr-gss-
c	756	19	0.8	598	9	CE444235	CE444235 tigr-gss-
	757	19	0.8	598	9	CE544529	CE544529 tigr-gss-
c	758	19	0.8	598	9	CE558372	CE558372 tigr-gss-
	759	19	0.8	598	9	CE809529	CE809529 tigr-gss-
c	760	19	0.8	600	5	BX327664	BX327664 BX327664
c	761	19	0.8	600	9	CE713589	CE713589 tigr-gss-
	762	19	0.8	601	9	CE078569	CE078569 tigr-gss-
	763	19	0.8	601	9	CE155131	CE155131 tigr-gss-
c	764	19	0.8	602	9	CE511272	CE511272 tigr-gss-
	765	19	0.8	603	4	BM487089	BM487089 pgm2n.pk0
c	766	19	0.8	603	9	CE564159	CE564159 tigr-gss-
	767	19	0.8	604	9	CE467854	CE467854 tigr-gss-
c	768	19	0.8	604	9	CE490884	CE490884 tigr-gss-
	769	19	0.8	604	9	CE533046	CE533046 tigr-gss-
c	770	19	0.8	605	9	CE005744	CE005744 tigr-gss-
	771	19	0.8	605	9	CE012459	CE012459 tigr-gss-
c	772	19	0.8	605	9	CE352503	CE352503 tigr-gss-
	773	19	0.8	606	8	BZ934083	BZ934083 CH240_89D
	774	19	0.8	606	9	CE409770	CE409770 tigr-gss-
	775	19	0.8	606	9	CE811508	CE811508 tigr-gss-
	776	19	0.8	607	9	CE785124	CE785124 tigr-gss-
	777	19	0.8	608	9	CE344087	CE344087 tigr-gss-
c	778	19	0.8	608	9	CE530810	CE530810 tigr-gss-
c	779	19	0.8	609	7	CF229247	CF229247 PtaXM0023
c	780	19	0.8	609	9	CE193971	CE193971 tigr-gss-
	781	19	0.8	609	9	CE270700	CE270700 tigr-gss-
	782	19	0.8	609	9	CE563973	CE563973 tigr-gss-
	783	19	0.8	610	9	CE215895	CE215895 tigr-gss-
	784	19	0.8	610	9	CE336647	CE336647 tigr-gss-
	785	19	0.8	610	9	CE703958	CE703958 tigr-gss-
c	786	19	0.8	611	8	BH086863	BH086863 RPCI-24-3
	787	19	0.8	611	9	CR296869	CR296869 Medicago
	788	19	0.8	611	9	CE060580	CE060580 tigr-gss-
c	789	19	0.8	611	9	CE404589	CE404589 tigr-gss-
c	790	19	0.8	611	9	CE502525	CE502525 tigr-gss-
c	791	19	0.8	611	9	CE723162	CE723162 tigr-gss-
	792	19	0.8	612	9	CE154696	CE154696 tigr-gss-
c	793	19	0.8	612	9	CE333461	CE333461 tigr-gss-
	794	19	0.8	613	9	CE171429	CE171429 tigr-gss-
	795	19	0.8	613	9	CE202458	CE202458 tigr-gss-
c	796	19	0.8	613	9	CE272758	CE272758 tigr-gss-
c	797	19	0.8	614	2	AW084703	AW084703 xa46e11.x
	798	19	0.8	614	5	BM944851	BM944851 UI-M-EH0p
	799	19	0.8	614	6	CA095251	CA095251 SCCCCL500
c	800	19	0.8	614	6	CD765300	CD765300 GGEZLB102
	801	19	0.8	614	8	BH031454	BH031454 RPCI-24-2
	802	19	0.8	614	9	CE068643	CE068643 tigr-gss-
c	803	19	0.8	614	9	CE206031	CE206031 tigr-gss-
c	804	19	0.8	614	9	CE353275	CE353275 tigr-gss-
c	805	19	0.8	615	9	CE042760	CE042760 tigr-gss-
	806	19	0.8	615	9	CE412403	CE412403 tigr-gss-

c 807	19	0.8	615	9	CE414297	CE414297 tigr-gss-
808	19	0.8	615	9	CE779412	CE779412 tigr-gss-
c 809	19	0.8	616	9	CE728853	CE728853 tigr-gss-
810	19	0.8	617	9	CE279831	CE279831 tigr-gss-
811	19	0.8	617	9	CE496887	CE496887 tigr-gss-
c 812	19	0.8	618	7	CN399820	CN399820 170004179
c 813	19	0.8	618	9	CE290403	CE290403 tigr-gss-
c 814	19	0.8	618	9	CE624805	CE624805 tigr-gss-
815	19	0.8	619	9	CE351280	CE351280 tigr-gss-
816	19	0.8	619	9	CE356630	CE356630 tigr-gss-
817	19	0.8	620	4	BM713814	BM713814 UI-E-EJ0-
c 818	19	0.8	620	9	CE837088	CE837088 tigr-gss-
c 819	19	0.8	621	5	BU704012	BU704012 UI-M-FO0-
820	19	0.8	621	7	CK332159	CK332159 H8192B02-
821	19	0.8	621	9	CE391609	CE391609 tigr-gss-
822	19	0.8	621	9	CE480466	CE480466 tigr-gss-
823	19	0.8	622	5	BU198134	BU198134 DCBCPD09
824	19	0.8	622	5	BU218077	BU218077 602883385
c 825	19	0.8	622	9	CE128017	CE128017 tigr-gss-
c 826	19	0.8	622	9	CE242081	CE242081 tigr-gss-
c 827	19	0.8	623	4	BG900730	BG900730 HOA6-1-E4
828	19	0.8	624	9	CE745905	CE745905 tigr-gss-
829	19	0.8	625	9	CE808290	CE808290 tigr-gss-
c 830	19	0.8	625	9	CE824882	CE824882 tigr-gss-
831	19	0.8	625	9	CG809240	CG809240 FSAAD79TR
c 832	19	0.8	626	9	CE115452	CE115452 tigr-gss-
c 833	19	0.8	626	9	CE340943	CE340943 tigr-gss-
834	19	0.8	626	9	CE356935	CE356935 tigr-gss-
835	19	0.8	628	9	CE429138	CE429138 tigr-gss-
c 836	19	0.8	628	9	CE697964	CE697964 tigr-gss-
c 837	19	0.8	628	9	CE796933	CE796933 tigr-gss-
838	19	0.8	629	9	CE852615	CE852615 tigr-gss-
839	19	0.8	630	9	CE181275	CE181275 tigr-gss-
840	19	0.8	630	9	CE654386	CE654386 tigr-gss-
c 841	19	0.8	630	9	CE749238	CE749238 tigr-gss-
842	19	0.8	631	7	CF361215	CF361215 827535 MA
c 843	19	0.8	631	9	CE402062	CE402062 tigr-gss-
844	19	0.8	631	9	CE750646	CE750646 tigr-gss-
845	19	0.8	631	9	CE843098	CE843098 tigr-gss-
c 846	19	0.8	632	9	CE244775	CE244775 tigr-gss-
c 847	19	0.8	632	9	CE363467	CE363467 tigr-gss-
c 848	19	0.8	632	9	CE436888	CE436888 tigr-gss-
849	19	0.8	633	6	CB816957	CB816957 dlg19pz.r
c 850	19	0.8	633	8	AQ535941	AQ535941 RPCI-11-3
c 851	19	0.8	633	9	DR10I23S	AL749388 Danio rer
c 852	19	0.8	633	9	CE011262	CE011262 tigr-gss-
853	19	0.8	633	9	CE155736	CE155736 tigr-gss-
854	19	0.8	633	9	CE322554	CE322554 tigr-gss-
c 855	19	0.8	633	9	CE762808	CE762808 tigr-gss-
c 856	19	0.8	634	9	CE734545	CE734545 tigr-gss-
c 857	19	0.8	635	8	AZ829791	AZ829791 2M0107G12
858	19	0.8	635	9	CE219653	CE219653 tigr-gss-
c 859	19	0.8	635	9	CE303021	CE303021 tigr-gss-
860	19	0.8	636	9	CE079408	CE079408 tigr-gss-
c 861	19	0.8	638	9	CE378056	CE378056 tigr-gss-
862	19	0.8	638	9	CE491764	CE491764 tigr-gss-
c 863	19	0.8	638	9	CE811142	CE811142 tigr-gss-

c 864	19	0.8	639	6	CB456756	CB456756 714048 MA
c 865	19	0.8	639	9	CE269872	CE269872 tigr-gss-
866	19	0.8	639	9	CE270215	CE270215 tigr-gss-
c 867	19	0.8	639	9	CE681402	CE681402 tigr-gss-
868	19	0.8	641	9	CE016761	CE016761 tigr-gss-
c 869	19	0.8	642	5	BX329667	BX329667 BX329667
c 870	19	0.8	642	9	CE071794	CE071794 tigr-gss-
c 871	19	0.8	642	9	CE363790	CE363790 tigr-gss-
c 872	19	0.8	642	9	CE473429	CE473429 tigr-gss-
c 873	19	0.8	642	9	CE535428	CE535428 tigr-gss-
874	19	0.8	642	9	CE675492	CE675492 tigr-gss-
875	19	0.8	642	9	CE751509	CE751509 tigr-gss-
876	19	0.8	642	9	CE759354	CE759354 tigr-gss-
877	19	0.8	642	9	CE780349	CE780349 tigr-gss-
c 878	19	0.8	643	6	CD094521	CD094521 ME1-0002G
879	19	0.8	643	9	CE040210	CE040210 tigr-gss-
880	19	0.8	643	9	CE515764	CE515764 tigr-gss-
881	19	0.8	643	9	CE579639	CE579639 tigr-gss-
c 882	19	0.8	643	9	CE678521	CE678521 tigr-gss-
c 883	19	0.8	643	9	CE834604	CE834604 tigr-gss-
884	19	0.8	644	5	BU364037	BU364037 603787470
c 885	19	0.8	644	9	CE751874	CE751874 tigr-gss-
c 886	19	0.8	645	9	CE191694	CE191694 tigr-gss-
c 887	19	0.8	645	9	CE268503	CE268503 tigr-gss-
c 888	19	0.8	645	9	CE427534	CE427534 tigr-gss-
889	19	0.8	646	4	BM167840	BM167840 EST570363
890	19	0.8	646	9	CE167458	CE167458 tigr-gss-
891	19	0.8	646	9	CE554899	CE554899 tigr-gss-
c 892	19	0.8	646	9	CE622412	CE622412 tigr-gss-
c 893	19	0.8	647	9	CE254453	CE254453 tigr-gss-
894	19	0.8	647	9	CE338170	CE338170 tigr-gss-
c 895	19	0.8	647	9	CE643803	CE643803 tigr-gss-
c 896	19	0.8	648	9	CE090826	CE090826 tigr-gss-
897	19	0.8	648	9	CE512282	CE512282 tigr-gss-
c 898	19	0.8	648	9	CE692179	CE692179 tigr-gss-
899	19	0.8	648	9	CE735931	CE735931 tigr-gss-
c 900	19	0.8	649	9	CE321965	CE321965 tigr-gss-
901	19	0.8	649	9	CE398244	CE398244 tigr-gss-
c 902	19	0.8	649	9	CE804754	CE804754 tigr-gss-
c 903	19	0.8	650	9	CE068478	CE068478 tigr-gss-
c 904	19	0.8	650	9	CE206106	CE206106 tigr-gss-
905	19	0.8	650	9	CE305824	CE305824 tigr-gss-
c 906	19	0.8	650	9	CE504643	CE504643 tigr-gss-
c 907	19	0.8	651	8	BZ251692	BZ251692 CH230-306
c 908	19	0.8	651	9	CE534710	CE534710 tigr-gss-
909	19	0.8	651	9	CE722648	CE722648 tigr-gss-
910	19	0.8	652	9	CE201197	CE201197 tigr-gss-
c 911	19	0.8	652	9	CE253757	CE253757 tigr-gss-
912	19	0.8	652	9	CE412769	CE412769 tigr-gss-
c 913	19	0.8	652	9	CE679728	CE679728 tigr-gss-
914	19	0.8	652	9	CE742518	CE742518 tigr-gss-
c 915	19	0.8	652	9	CE802303	CE802303 tigr-gss-
916	19	0.8	653	9	CE364543	CE364543 tigr-gss-
c 917	19	0.8	653	9	CE669274	CE669274 tigr-gss-
c 918	19	0.8	654	9	CL348273	CL348273 RPCI44_27
919	19	0.8	656	9	CE225195	CE225195 tigr-gss-
c 920	19	0.8	656	9	CE317406	CE317406 tigr-gss-

	921	19	0.8	657	6	CA160888 CA160888 SCMCRZ306
	922	19	0.8	657	9	CE227726 CE227726 tigr-gss-
	923	19	0.8	658	9	CE262800 CE262800 tigr-gss-
c	924	19	0.8	658	9	CE301824 CE301824 tigr-gss-
	925	19	0.8	658	9	CE312659 CE312659 tigr-gss-
c	926	19	0.8	658	9	CE408208 CE408208 tigr-gss-
c	927	19	0.8	658	9	CE775750 CE775750 tigr-gss-
	928	19	0.8	659	9	CE122998 CE122998 tigr-gss-
	929	19	0.8	659	9	CE327319 CE327319 tigr-gss-
c	930	19	0.8	659	9	CE467179 CE467179 tigr-gss-
c	931	19	0.8	659	9	CE492930 CE492930 tigr-gss-
	932	19	0.8	659	9	CE502144 CE502144 tigr-gss-
	933	19	0.8	659	9	CE595018 CE595018 tigr-gss-
	934	19	0.8	660	5	BX404563 BX404563 BX404563
c	935	19	0.8	660	6	BY726304 BY726304 BY726304
	936	19	0.8	660	9	CE336605 CE336605 tigr-gss-
	937	19	0.8	660	9	CE345583 CE345583 tigr-gss-
c	938	19	0.8	660	9	CE400122 CE400122 tigr-gss-
	939	19	0.8	660	9	CE818444 CE818444 tigr-gss-
c	940	19	0.8	660	9	CE823742 CE823742 tigr-gss-
c	941	19	0.8	661	5	BU298539 BU298539 603740493
	942	19	0.8	661	8	BZ306400 BZ306400 hx42b11.b
	943	19	0.8	661	9	CE110665 CE110665 tigr-gss-
	944	19	0.8	661	9	CE383364 CE383364 tigr-gss-
	945	19	0.8	662	9	CE025178 CE025178 tigr-gss-
	946	19	0.8	662	9	CE519195 CE519195 tigr-gss-
c	947	19	0.8	663	8	BH503885 BH503885 BOHQJ43TR
	948	19	0.8	663	9	CE408699 CE408699 tigr-gss-
c	949	19	0.8	663	9	CE412381 CE412381 tigr-gss-
c	950	19	0.8	663	9	CE472613 CE472613 tigr-gss-
	951	19	0.8	664	6	CA196760 CA196760 SCBFAD109
	952	19	0.8	664	9	CE142136 CE142136 tigr-gss-
c	953	19	0.8	664	9	CE614068 CE614068 tigr-gss-
	954	19	0.8	665	9	AG088250 AG088250 Pan trogl
c	955	19	0.8	665	9	CE203400 CE203400 tigr-gss-
c	956	19	0.8	665	9	CE574445 CE574445 tigr-gss-
c	957	19	0.8	665	9	CE619544 CE619544 tigr-gss-
	958	19	0.8	665	9	CE809413 CE809413 tigr-gss-
c	959	19	0.8	665	9	CE839530 CE839530 tigr-gss-
c	960	19	0.8	666	2	BE855330 BE855330 ux51d10.y
c	961	19	0.8	666	4	BI091323 BI091323 602855975
c	962	19	0.8	666	9	CE216908 CE216908 tigr-gss-
c	963	19	0.8	666	9	CE400580 CE400580 tigr-gss-
c	964	19	0.8	666	9	CE460531 CE460531 tigr-gss-
	965	19	0.8	666	9	CE643877 CE643877 tigr-gss-
	966	19	0.8	667	9	CE010806 CE010806 tigr-gss-
c	967	19	0.8	667	9	CE175489 CE175489 tigr-gss-
	968	19	0.8	667	9	CE195965 CE195965 tigr-gss-
	969	19	0.8	667	9	CE339784 CE339784 tigr-gss-
	970	19	0.8	667	9	CE630767 CE630767 tigr-gss-
	971	19	0.8	668	9	CE297162 CE297162 tigr-gss-
c	972	19	0.8	668	9	CE718910 CE718910 tigr-gss-
c	973	19	0.8	668	9	CE773634 CE773634 tigr-gss-
c	974	19	0.8	669	9	CE216980 CE216980 tigr-gss-
	975	19	0.8	669	9	CE315422 CE315422 tigr-gss-
c	976	19	0.8	669	9	CE750235 CE750235 tigr-gss-
c	977	19	0.8	669	9	CE825783 CE825783 tigr-gss-

c 978	19	0.8	670	9	CE618606	CE618606 tigr-gss-
c 979	19	0.8	671	7	CF785111	CF785111 AGENCOURT
c 980	19	0.8	671	9	CE271149	CE271149 tigr-gss-
c 981	19	0.8	671	9	CE272053	CE272053 tigr-gss-
982	19	0.8	671	9	CE343728	CE343728 tigr-gss-
983	19	0.8	671	9	CE831211	CE831211 tigr-gss-
984	19	0.8	672	8	BZ888251	BZ888251 CH240_257
c 985	19	0.8	672	9	CE018311	CE018311 tigr-gss-
c 986	19	0.8	672	9	CE784985	CE784985 tigr-gss-
987	19	0.8	672	9	CE787256	CE787256 tigr-gss-
988	19	0.8	673	6	CA812819	CA812819 CA48LN07I
989	19	0.8	673	9	BX971452	BX971452 Reverse s
990	19	0.8	673	9	CE112904	CE112904 tigr-gss-
c 991	19	0.8	673	9	CE124149	CE124149 tigr-gss-
992	19	0.8	673	9	CE428929	CE428929 tigr-gss-
993	19	0.8	674	9	CE595808	CE595808 tigr-gss-
c 994	19	0.8	674	9	CE809245	CE809245 tigr-gss-
c 995	19	0.8	674	9	CE847253	CE847253 tigr-gss-
996	19	0.8	675	9	AG043938	AG043938 Pan trogl
c 997	19	0.8	675	9	AG172133	AG172133 Pan trogl
c 998	19	0.8	676	7	CF113151	CF113151 Shultzomi
c 999	19	0.8	676	7	CN413937	CN413937 170005328
c1000	19	0.8	676	9	AG119646	AG119646 Pan trogl
1001	19	0.8	676	9	CE055616	CE055616 tigr-gss-
c1002	19	0.8	676	9	CE087647	CE087647 tigr-gss-
1003	19	0.8	676	9	CE409441	CE409441 tigr-gss-
c1004	19	0.8	676	9	CE443438	CE443438 tigr-gss-
1005	19	0.8	677	8	BH998337	BH998337 oei85f05.
1006	19	0.8	677	9	CE193106	CE193106 tigr-gss-
1007	19	0.8	677	9	CE284108	CE284108 tigr-gss-
1008	19	0.8	677	9	CE473122	CE473122 tigr-gss-
c1009	19	0.8	677	9	CE696564	CE696564 tigr-gss-
1010	19	0.8	678	5	BU235195	BU235195 603792853
c1011	19	0.8	678	9	CE283255	CE283255 tigr-gss-
c1012	19	0.8	678	9	CE622999	CE622999 tigr-gss-
1013	19	0.8	678	9	CE694742	CE694742 tigr-gss-
c1014	19	0.8	679	9	CE544794	CE544794 tigr-gss-
c1015	19	0.8	680	6	CB169100	CB169100 IMU602702
1016	19	0.8	680	8	BZ087618	BZ087618 1kg67h10.
1017	19	0.8	680	9	CE093549	CE093549 tigr-gss-
1018	19	0.8	680	9	CE288191	CE288191 tigr-gss-
c1019	19	0.8	680	9	CE724945	CE724945 tigr-gss-
1020	19	0.8	680	9	CE771859	CE771859 tigr-gss-
c1021	19	0.8	681	7	CK748526	CK748526 pam01-1ms
1022	19	0.8	681	9	CE103692	CE103692 tigr-gss-
c1023	19	0.8	681	9	CE192506	CE192506 tigr-gss-
c1024	19	0.8	681	9	CE195317	CE195317 tigr-gss-
1025	19	0.8	681	9	CE517696	CE517696 tigr-gss-
c1026	19	0.8	681	9	CE560119	CE560119 tigr-gss-
c1027	19	0.8	681	9	CE676880	CE676880 tigr-gss-
c1028	19	0.8	682	6	CA374470	CA374470 648902 NC
1029	19	0.8	682	9	CE565033	CE565033 tigr-gss-
c1030	19	0.8	683	7	CF235569	CF235569 PtaJXT002
c1031	19	0.8	683	9	AG211589	AG211589 Oryza sat
c1032	19	0.8	683	9	CE251727	CE251727 tigr-gss-
1033	19	0.8	683	9	CE489518	CE489518 tigr-gss-
c1034	19	0.8	683	9	CE494365	CE494365 tigr-gss-

c1035	19	0.8	684	6	BY720132	BY720132 BY720132
1036	19	0.8	684	9	CE057124	CE057124 tigr-gss-
1037	19	0.8	684	9	CE207772	CE207772 tigr-gss-
c1038	19	0.8	684	9	CE345446	CE345446 tigr-gss-
c1039	19	0.8	685	9	CR127048	CR127048 Reverse s
1040	19	0.8	685	9	CE607430	CE607430 tigr-gss-
c1041	19	0.8	685	9	CE847625	CE847625 tigr-gss-
1042	19	0.8	686	6	CA291576	CA291576 SCCCNR100
1043	19	0.8	686	6	CD728541	CD728541 4034413 1
1044	19	0.8	686	8	BH942339	BH942339 odg48d04.
1045	19	0.8	686	9	CE069483	CE069483 tigr-gss-
1046	19	0.8	686	9	CE296171	CE296171 tigr-gss-
1047	19	0.8	686	9	CE542430	CE542430 tigr-gss-
1048	19	0.8	686	9	CE791904	CE791904 tigr-gss-
c1049	19	0.8	687	7	CN399821	CN399821 170004251
1050	19	0.8	687	8	B76321	B76321 RPCI11-14O1
1051	19	0.8	687	8	BH996696	BH996696 oef89c08.
c1052	19	0.8	688	9	CE096962	CE096962 tigr-gss-
1053	19	0.8	688	9	CE357514	CE357514 tigr-gss-
1054	19	0.8	689	8	BZ935402	BZ935402 CH240_85A
1055	19	0.8	689	9	CE190232	CE190232 tigr-gss-
c1056	19	0.8	689	9	CE209595	CE209595 tigr-gss-
1057	19	0.8	689	9	CE438037	CE438037 tigr-gss-
1058	19	0.8	689	9	CE763734	CE763734 tigr-gss-
1059	19	0.8	690	7	CR754500	CR754500 CR754500
c1060	19	0.8	690	7	CR755770	CR755770 CR755770
c1061	19	0.8	690	8	AZ979594	AZ979594 2M0256P14
1062	19	0.8	690	8	BH932541	BH932541 odh46h01.
c1063	19	0.8	690	9	CE072967	CE072967 tigr-gss-
1064	19	0.8	690	9	CE076568	CE076568 tigr-gss-
c1065	19	0.8	690	9	CE103838	CE103838 tigr-gss-
c1066	19	0.8	690	9	CE118541	CE118541 tigr-gss-
c1067	19	0.8	690	9	CE155228	CE155228 tigr-gss-
c1068	19	0.8	690	9	CE162930	CE162930 tigr-gss-
c1069	19	0.8	690	9	CE187076	CE187076 tigr-gss-
1070	19	0.8	690	9	CE421217	CE421217 tigr-gss-
c1071	19	0.8	690	9	CE583386	CE583386 tigr-gss-
c1072	19	0.8	690	9	CE622192	CE622192 tigr-gss-
1073	19	0.8	691	9	CE058472	CE058472 tigr-gss-
1074	19	0.8	691	9	CE125003	CE125003 tigr-gss-
c1075	19	0.8	691	9	CE371066	CE371066 tigr-gss-
1076	19	0.8	691	9	CE843985	CE843985 tigr-gss-
c1077	19	0.8	692	5	BU005981	BU005981 QGG9J22.y
c1078	19	0.8	692	8	BH998217	BH998217 oed82d11.
c1079	19	0.8	692	9	CE077826	CE077826 tigr-gss-
1080	19	0.8	692	9	CE190755	CE190755 tigr-gss-
c1081	19	0.8	692	9	CE339383	CE339383 tigr-gss-
c1082	19	0.8	693	9	CE328968	CE328968 tigr-gss-
1083	19	0.8	693	9	CE643726	CE643726 tigr-gss-
1084	19	0.8	693	9	CE770048	CE770048 tigr-gss-
1085	19	0.8	693	9	CE842871	CE842871 tigr-gss-
1086	19	0.8	694	9	CE460176	CE460176 tigr-gss-
c1087	19	0.8	694	9	CE726688	CE726688 tigr-gss-
c1088	19	0.8	695	9	CE222639	CE222639 tigr-gss-
c1089	19	0.8	695	9	CE355064	CE355064 tigr-gss-
c1090	19	0.8	695	9	CE764235	CE764235 tigr-gss-
c1091	19	0.8	696	9	CE059559	CE059559 tigr-gss-

1092	19	0.8	696	9	CE442615	CE442615 tigr-gss-
1093	19	0.8	696	9	CE649986	CE649986 tigr-gss-
c1094	19	0.8	696	9	CE706630	CE706630 tigr-gss-
1095	19	0.8	697	9	CNS0485I	AL278847 Tetraodon
c1096	19	0.8	697	9	CE601022	CE601022 tigr-gss-
1097	19	0.8	697	9	CE836969	CE836969 tigr-gss-
1098	19	0.8	698	8	BH979207	BH979207 ode94c03.
c1099	19	0.8	698	9	CE181348	CE181348 tigr-gss-
c1100	19	0.8	699	9	CE143497	CE143497 tigr-gss-
1101	19	0.8	699	9	CE665692	CE665692 tigr-gss-
c1102	19	0.8	699	9	CE818161	CE818161 tigr-gss-
1103	19	0.8	700	8	BZ419915	BZ419915 if61h03.b
c1104	19	0.8	700	9	CE071758	CE071758 tigr-gss-
c1105	19	0.8	700	9	CE163684	CE163684 tigr-gss-
1106	19	0.8	701	8	BH928951	BH928951 odh29f05.
c1107	19	0.8	701	8	BH940396	BH940396 odf76b09.
1108	19	0.8	701	9	CE786141	CE786141 tigr-gss-
1109	19	0.8	702	6	CD906384	CD906384 G468.104L
c1110	19	0.8	702	9	CE073757	CE073757 tigr-gss-
1111	19	0.8	702	9	CE177133	CE177133 tigr-gss-
c1112	19	0.8	702	9	CE543289	CE543289 tigr-gss-
c1113	19	0.8	703	9	CE442264	CE442264 tigr-gss-
1114	19	0.8	703	9	CE505523	CE505523 tigr-gss-
c1115	19	0.8	703	9	CE561655	CE561655 tigr-gss-
1116	19	0.8	704	8	AZ993875	AZ993875 2M0279P06
c1117	19	0.8	704	9	CE100432	CE100432 tigr-gss-
1118	19	0.8	704	9	CE537407	CE537407 tigr-gss-
c1119	19	0.8	704	9	CE552328	CE552328 tigr-gss-
c1120	19	0.8	704	9	CE651429	CE651429 tigr-gss-
c1121	19	0.8	705	5	BU224882	BU224882 603801186
1122	19	0.8	705	9	CE039952	CE039952 tigr-gss-
c1123	19	0.8	705	9	CE207786	CE207786 tigr-gss-
c1124	19	0.8	705	9	CE422051	CE422051 tigr-gss-
1125	19	0.8	705	9	CE445743	CE445743 tigr-gss-
c1126	19	0.8	705	9	CE553023	CE553023 tigr-gss-
c1127	19	0.8	705	9	CE582192	CE582192 tigr-gss-
c1128	19	0.8	706	9	CE035700	CE035700 tigr-gss-
1129	19	0.8	706	9	CE278911	CE278911 tigr-gss-
c1130	19	0.8	706	9	CE469153	CE469153 tigr-gss-
c1131	19	0.8	706	9	CE696467	CE696467 tigr-gss-
1132	19	0.8	708	4	BJ791749	BJ791749 BJ791749
c1133	19	0.8	708	6	BY729901	BY729901 BY729901
c1134	19	0.8	708	9	CE205928	CE205928 tigr-gss-
c1135	19	0.8	709	5	BM978029	BM978029 UI-CF-EC1
c1136	19	0.8	709	9	CE003499	CE003499 tigr-gss-
1137	19	0.8	709	9	CE372392	CE372392 tigr-gss-
c1138	19	0.8	709	9	CE415609	CE415609 tigr-gss-
1139	19	0.8	709	9	CE462458	CE462458 tigr-gss-
1140	19	0.8	710	4	BJ782535	BJ782535 BJ782535
1141	19	0.8	710	8	BZ072320	BZ072320 1ke36e07.
1142	19	0.8	710	9	CE318529	CE318529 tigr-gss-
c1143	19	0.8	710	9	CE637142	CE637142 tigr-gss-
c1144	19	0.8	711	9	CE035077	CE035077 tigr-gss-
1145	19	0.8	711	9	CE313950	CE313950 tigr-gss-
1146	19	0.8	712	8	BH932000	BH932000 odj16d03.
1147	19	0.8	712	9	CE135206	CE135206 tigr-gss-
c1148	19	0.8	712	9	CE165873	CE165873 tigr-gss-

c1149	19	0.8	712	9	CE302854	CE302854 tigr-gss-
1150	19	0.8	712	9	CE811643	CE811643 tigr-gss-
c1151	19	0.8	712	9	CE827426	CE827426 tigr-gss-
1152	19	0.8	713	6	BY732332	BY732332 BY732332
c1153	19	0.8	713	8	BZ027265	BZ027265 oeh17f05.
1154	19	0.8	713	9	CE053592	CE053592 tigr-gss-
c1155	19	0.8	713	9	CE214862	CE214862 tigr-gss-
c1156	19	0.8	713	9	CE217260	CE217260 tigr-gss-
1157	19	0.8	713	9	CE366448	CE366448 tigr-gss-
1158	19	0.8	713	9	CE393829	CE393829 tigr-gss-
1159	19	0.8	713	9	CE457088	CE457088 tigr-gss-
1160	19	0.8	713	9	CE668075	CE668075 tigr-gss-
c1161	19	0.8	714	7	CN296741	CN296741 170004706
c1162	19	0.8	714	9	CE272707	CE272707 tigr-gss-
c1163	19	0.8	714	9	CE717136	CE717136 tigr-gss-
1164	19	0.8	714	9	CE749086	CE749086 tigr-gss-
1165	19	0.8	714	9	CE804604	CE804604 tigr-gss-
1166	19	0.8	714	9	CE808542	CE808542 tigr-gss-
c1167	19	0.8	714	9	CE851635	CE851635 tigr-gss-
c1168	19	0.8	715	9	AG406459	AG406459 Mus muscu
c1169	19	0.8	715	9	CE494450	CE494450 tigr-gss-
c1170	19	0.8	715	9	CE767498	CE767498 tigr-gss-
c1171	19	0.8	716	5	BU247361	BU247361 603592373
c1172	19	0.8	716	7	CR285236	CR285236 CR285236
c1173	19	0.8	716	9	CC498059	CC498059 CH240_335
c1174	19	0.8	716	9	CE302113	CE302113 tigr-gss-
1175	19	0.8	716	9	CE573156	CE573156 tigr-gss-
1176	19	0.8	717	8	BH597760	BH597760 BOGMV30TR
c1177	19	0.8	717	9	CE077191	CE077191 tigr-gss-
c1178	19	0.8	718	9	CE364041	CE364041 tigr-gss-
c1179	19	0.8	719	9	AG415998	AG415998 Mus muscu
1180	19	0.8	719	9	CE287399	CE287399 tigr-gss-
c1181	19	0.8	719	9	CE347083	CE347083 tigr-gss-
c1182	19	0.8	720	9	CE078107	CE078107 tigr-gss-
c1183	19	0.8	720	9	CE153698	CE153698 tigr-gss-
c1184	19	0.8	720	9	CE190397	CE190397 tigr-gss-
c1185	19	0.8	720	9	CE486019	CE486019 tigr-gss-
c1186	19	0.8	720	9	CE576256	CE576256 tigr-gss-
1187	19	0.8	721	9	CE139984	CE139984 tigr-gss-
c1188	19	0.8	721	9	CE157771	CE157771 tigr-gss-
c1189	19	0.8	721	9	CE649902	CE649902 tigr-gss-
1190	19	0.8	722	9	CC567481	CC567481 CH240_441
c1191	19	0.8	722	9	CE276893	CE276893 tigr-gss-
c1192	19	0.8	722	9	CE385019	CE385019 tigr-gss-
c1193	19	0.8	723	8	BH670086	BH670086 BOHSR07TF
c1194	19	0.8	723	9	CE015839	CE015839 tigr-gss-
1195	19	0.8	723	9	CE118039	CE118039 tigr-gss-
c1196	19	0.8	723	9	CE418337	CE418337 tigr-gss-
c1197	19	0.8	723	9	CE771675	CE771675 tigr-gss-
c1198	19	0.8	724	9	CE438264	CE438264 tigr-gss-
c1199	19	0.8	725	9	CE087038	CE087038 tigr-gss-
c1200	19	0.8	725	9	CE104319	CE104319 tigr-gss-
c1201	19	0.8	725	9	CE474110	CE474110 tigr-gss-
c1202	19	0.8	725	9	CE624683	CE624683 tigr-gss-
c1203	19	0.8	725	9	CE742506	CE742506 tigr-gss-
c1204	19	0.8	726	5	BX956930	BX956930 DKFZp781C
1205	19	0.8	726	8	BH461010	BH461010 BOGBO64TR

c1206	19	0.8	727	9	CE389906	CE389906 tigr-gss-
c1207	19	0.8	727	9	CE715279	CE715279 tigr-gss-
c1208	19	0.8	727	9	CE734942	CE734942 tigr-gss-
c1209	19	0.8	727	9	CE749709	CE749709 tigr-gss-
c1210	19	0.8	727	9	CE776259	CE776259 tigr-gss-
c1211	19	0.8	728	8	BZ434030	BZ434030 BONAF08TR
c1212	19	0.8	728	8	BZ497694	BZ497694 BONMW83TF
c1213	19	0.8	728	9	CE081289	CE081289 tigr-gss-
c1214	19	0.8	728	9	CE210294	CE210294 tigr-gss-
c1215	19	0.8	728	9	CE326692	CE326692 tigr-gss-
c1216	19	0.8	728	9	CE756238	CE756238 tigr-gss-
c1217	19	0.8	728	9	CE769128	CE769128 tigr-gss-
1218	19	0.8	729	8	BH703303	BH703303 BOHUY82TR
c1219	19	0.8	729	9	CE140951	CE140951 tigr-gss-
c1220	19	0.8	729	9	CE231955	CE231955 tigr-gss-
1221	19	0.8	729	9	CE351162	CE351162 tigr-gss-
1222	19	0.8	729	9	CE443696	CE443696 tigr-gss-
c1223	19	0.8	729	9	CE676503	CE676503 tigr-gss-
c1224	19	0.8	730	6	CD906841	CD906841 G468.105J
1225	19	0.8	730	9	AG403799	AG403799 Mus muscu
c1226	19	0.8	730	9	CE059978	CE059978 tigr-gss-
1227	19	0.8	730	9	CE618099	CE618099 tigr-gss-
c1228	19	0.8	731	5	BU285139	BU285139 603864696
c1229	19	0.8	731	9	AG433363	AG433363 Mus muscu
1230	19	0.8	731	9	CR800768	CR800768 GR0AAA2CA
c1231	19	0.8	731	9	CE017092	CE017092 tigr-gss-
c1232	19	0.8	731	9	CE608851	CE608851 tigr-gss-
c1233	19	0.8	731	9	CE802753	CE802753 tigr-gss-
c1234	19	0.8	732	9	CE098234	CE098234 tigr-gss-
1235	19	0.8	732	9	CE187621	CE187621 tigr-gss-
c1236	19	0.8	732	9	CE843130	CE843130 tigr-gss-
1237	19	0.8	733	8	BH992753	BH992753 oed84d01.
1238	19	0.8	733	8	BZ485635	BZ485635 BONRP37TR
c1239	19	0.8	733	9	CE049548	CE049548 tigr-gss-
c1240	19	0.8	734	4	BG719818	BG719818 602691226
c1241	19	0.8	734	9	CE591681	CE591681 tigr-gss-
c1242	19	0.8	735	9	CE684232	CE684232 tigr-gss-
c1243	19	0.8	735	9	CG342154	CG342154 OGVGC47TH
c1244	19	0.8	736	9	CE786200	CE786200 tigr-gss-
1245	19	0.8	737	7	CO567098	CO567098 AGENCOURT
c1246	19	0.8	737	9	CE659849	CE659849 tigr-gss-
1247	19	0.8	738	9	CE327604	CE327604 tigr-gss-
c1248	19	0.8	739	9	CE192890	CE192890 tigr-gss-
c1249	19	0.8	739	9	CE340404	CE340404 tigr-gss-
c1250	19	0.8	739	9	CE458130	CE458130 tigr-gss-
c1251	19	0.8	739	9	CE779095	CE779095 tigr-gss-
c1252	19	0.8	740	9	CE302237	CE302237 tigr-gss-
c1253	19	0.8	741	8	BH606419	BH606419 BOGFM10TR
c1254	19	0.8	741	8	BH937592	BH937592 odg57e02.
1255	19	0.8	741	8	AQ582716	AQ582716 RPCI-11-4
c1256	19	0.8	741	9	CE351502	CE351502 tigr-gss-
c1257	19	0.8	741	9	CE493127	CE493127 tigr-gss-
c1258	19	0.8	741	9	CE623526	CE623526 tigr-gss-
c1259	19	0.8	742	9	CE590970	CE590970 tigr-gss-
c1260	19	0.8	743	9	CE157867	CE157867 tigr-gss-
c1261	19	0.8	743	9	CE291430	CE291430 tigr-gss-
1262	19	0.8	743	9	CE827492	CE827492 tigr-gss-

c1263	19	0.8	744	9	CE386062	CE386062 tigr-gss-
c1264	19	0.8	744	9	CE426947	CE426947 tigr-gss-
1265	19	0.8	744	9	CE573679	CE573679 tigr-gss-
c1266	19	0.8	745	9	CE122468	CE122468 tigr-gss-
c1267	19	0.8	745	9	CE747647	CE747647 tigr-gss-
c1268	19	0.8	746	9	AG454470	AG454470 Mus muscu
c1269	19	0.8	746	9	AG571147	AG571147 Mus muscu
c1270	19	0.8	746	9	CE429845	CE429845 tigr-gss-
c1271	19	0.8	746	9	CE468182	CE468182 tigr-gss-
1272	19	0.8	746	9	CE573824	CE573824 tigr-gss-
1273	19	0.8	747	9	CE121743	CE121743 tigr-gss-
c1274	19	0.8	747	9	CE123201	CE123201 tigr-gss-
1275	19	0.8	748	8	BZ396654	BZ396654 EINAQ56TR
c1276	19	0.8	748	9	AG492780	AG492780 Mus muscu
1277	19	0.8	748	9	CE218398	CE218398 tigr-gss-
c1278	19	0.8	748	9	CE457596	CE457596 tigr-gss-
1279	19	0.8	749	9	CE224436	CE224436 tigr-gss-
1280	19	0.8	750	8	BH122972	BH122972 RPCI-24-2
c1281	19	0.8	750	9	CE471066	CE471066 tigr-gss-
c1282	19	0.8	750	9	CE779100	CE779100 tigr-gss-
c1283	19	0.8	750	9	CE847179	CE847179 tigr-gss-
c1284	19	0.8	751	9	CE799085	CE799085 tigr-gss-
c1285	19	0.8	752	7	CK474028	CK474028 AGENCOURT
c1286	19	0.8	752	9	CE052741	CE052741 tigr-gss-
c1287	19	0.8	752	9	CE108352	CE108352 tigr-gss-
1288	19	0.8	752	9	CE132472	CE132472 tigr-gss-
c1289	19	0.8	752	9	CE323070	CE323070 tigr-gss-
c1290	19	0.8	753	9	CE330308	CE330308 tigr-gss-
c1291	19	0.8	754	5	BU260339	BU260339 603502283
1292	19	0.8	755	4	BJ795984	BJ795984 BJ795984
1293	19	0.8	755	9	CL750592	CL750592 OR_BBa011
c1294	19	0.8	756	9	AG589902	AG589902 Mus muscu
c1295	19	0.8	756	9	CE683828	CE683828 tigr-gss-
c1296	19	0.8	757	8	BZ502888	BZ502888 BONMK14TR
1297	19	0.8	758	4	BI819345	BI819345 603034505
c1298	19	0.8	758	8	BH924361	BH924361 odi55a04.
c1299	19	0.8	760	8	BH478501	BH478501 BOHAJ54TR
c1300	19	0.8	760	9	CE576742	CE576742 tigr-gss-
c1301	19	0.8	761	8	AZ623852	AZ623852 1M0462A03
1302	19	0.8	761	8	BZ060851	BZ060851 lju10b03.
c1303	19	0.8	761	9	CE291455	CE291455 tigr-gss-
c1304	19	0.8	763	9	CR275365	CR275365 Reverse s
c1305	19	0.8	763	9	CE375441	CE375441 tigr-gss-
c1306	19	0.8	763	9	CE432049	CE432049 tigr-gss-
c1307	19	0.8	764	9	AG487347	AG487347 Mus muscu
c1308	19	0.8	764	9	CE062499	CE062499 tigr-gss-
c1309	19	0.8	764	9	CE331849	CE331849 tigr-gss-
c1310	19	0.8	766	9	CE280593	CE280593 tigr-gss-
c1311	19	0.8	766	9	CE569560	CE569560 tigr-gss-
1312	19	0.8	767	5	BU854442	BU854442 AGENCOURT
1313	19	0.8	767	9	CE086450	CE086450 tigr-gss-
c1314	19	0.8	767	9	CE717068	CE717068 tigr-gss-
1315	19	0.8	768	8	BZ180286	BZ180286 CH230-434
c1316	19	0.8	768	9	CE308947	CE308947 tigr-gss-
c1317	19	0.8	769	9	CE238714	CE238714 tigr-gss-
c1318	19	0.8	770	9	CE317307	CE317307 tigr-gss-
c1319	19	0.8	771	9	CE246607	CE246607 tigr-gss-

c1320	19	0.8	773	9	CE827643	CE827643 tigr-gss-
1321	19	0.8	774	4	BG753925	BG753925 602709446
1322	19	0.8	774	8	BH478920	BH478920 BOGWN41TR
c1323	19	0.8	775	9	AG523838	AG523838 Mus muscu
c1324	19	0.8	776	9	CL135735	CL135735 ISB1-106P
1325	19	0.8	777	9	CE730042	CE730042 tigr-gss-
c1326	19	0.8	779	9	CR823371	CR823371 GR0AAA53C
c1327	19	0.8	779	9	CE026588	CE026588 tigr-gss-
c1328	19	0.8	780	9	CR274821	CR274821 Forward s
c1329	19	0.8	781	5	BU465345	BU465345 603369485
1330	19	0.8	781	8	BZ392975	BZ392975 EINAM01TF
1331	19	0.8	781	8	BZ610446	BZ610446 WHACW68TR
c1332	19	0.8	782	9	CE404635	CE404635 tigr-gss-
1333	19	0.8	783	7	CO363325	CO363325 RTK1_9_B1
1334	19	0.8	783	8	BZ513134	BZ513134 BOMQL26TF
1335	19	0.8	785	8	BH726536	BH726536 BOMDR44TF
1336	19	0.8	786	9	CE820882	CE820882 tigr-gss-
c1337	19	0.8	788	9	CR257365	CR257365 Reverse s
1338	19	0.8	793	7	CF256209	CF256209 mdvn137_b
c1339	19	0.8	794	5	BU382423	BU382423 603861509
c1340	19	0.8	797	5	BP163963	BP163963 BP163963
1341	19	0.8	797	8	BZ410657	BZ410657 OGACC75TM
1342	19	0.8	798	2	BE544133	BE544133 601076669
1343	19	0.8	798	5	BQ687097	BQ687097 AGENCOURT
c1344	19	0.8	799	5	BU327530	BU327530 603406292
c1345	19	0.8	800	4	BG167946	BG167946 602340041
1346	19	0.8	802	4	BM162880	BM162880 EST565403
1347	19	0.8	802	4	BM164694	BM164694 EST567217
c1348	19	0.8	804	9	CG175327	CG175327 PUIEO44TD
1349	19	0.8	804	9	CG966119	CG966119 MBEIB41TF
c1350	19	0.8	805	9	CR230142	CR230142 Forward s
c1351	19	0.8	805	9	CL957676	CL957676 OsIRUA000
c1352	19	0.8	806	6	CA266956	CA266956 SCRFLB206
1353	19	0.8	806	7	CK196084	CK196084 FGAS00453
1354	19	0.8	807	6	CA812768	CA812768 CA48LN07I
1355	19	0.8	809	8	BH649410	BH649410 BOMAF05TF
1356	19	0.8	810	9	CR274398	CR274398 Reverse s
c1357	19	0.8	812	4	BI758489	BI758489 603023334
c1358	19	0.8	814	8	BH573522	BH573522 BOGYW17TF
1359	19	0.8	816	8	CC395073	CC395073 PUHAY16TD
c1360	19	0.8	817	4	BM360844	BM360844 GA__Ea003
c1361	19	0.8	817	8	BZ246890	BZ246890 CH230-325
c1362	19	0.8	817	9	CR114033	CR114033 Reverse s
1363	19	0.8	818	4	BI732082	BI732082 603352870
c1364	19	0.8	818	9	CR033021	CR033021 Reverse s
1365	19	0.8	819	7	CK238077	CK238077 AGENCOURT
1366	19	0.8	819	8	CC199510	CC199510 ZMMBBc032
1367	19	0.8	820	8	BZ471347	BZ471347 BONGV68TF
1368	19	0.8	820	9	CC805897	CC805897 ZMMBBc046
c1369	19	0.8	822	9	CL301194	CL301194 gbs08_CH2
c1370	19	0.8	823	5	BU362418	BU362418 603784642
1371	19	0.8	826	7	CV471435	CV471435 44596.1 C
1372	19	0.8	827	7	CN823337	CN823337 Oa_splbn_
c1373	19	0.8	830	9	CR094185	CR094185 Reverse s
c1374	19	0.8	832	5	BU420520	BU420520 603955117
c1375	19	0.8	833	8	BH463106	BH463106 BOGZV24TR
1376	19	0.8	836	7	CK197204	CK197204 FGAS00567

1377	19	0.8	836	7	CK395412	CK395412 AGENCOURT
c1378	19	0.8	837	8	BH535517	BH535517 BOHOK70TF
c1379	19	0.8	837	8	BH594142	BH594142 BOGWZ48TF
1380	19	0.8	838	8	BH709341	BH709341 BOHXS96TF
c1381	19	0.8	839	7	CO485027	CO485027 GQ0206.TB
1382	19	0.8	840	9	CC720879	CC720879 OGMAV35TH
1383	19	0.8	844	6	CD325893	CD325893 AGENCOURT
c1384	19	0.8	845	9	CR135205	CR135205 Reverse s
c1385	19	0.8	848	6	CD643411	CD643411 AGENCOURT
1386	19	0.8	853	8	BH705190	BH705190 BOHUS10TF
c1387	19	0.8	853	8	BZ410652	BZ410652 OGACC75TC
c1388	19	0.8	853	8	CC395070	CC395070 PUHAY16TB
c1389	19	0.8	855	9	CG008314	CG008314 ZUAAM10TH
1390	19	0.8	858	7	CV236957	CV236957 WS01226.B
1391	19	0.8	860	8	AZ046318	AZ046318 nbeb0091P
1392	19	0.8	860	8	BZ224049	BZ224049 CH230-260
c1393	19	0.8	862	9	BX988666	BX988666 Reverse s
1394	19	0.8	866	8	BH596501	BH596501 BOGZY74TF
c1395	19	0.8	866	8	BH720198	BH720198 BOHZV36TF
c1396	19	0.8	867	8	BZ640953	BZ640953 OGCAX06TC
1397	19	0.8	868	9	CNS01NIT	AL152278 Anopheles
c1398	19	0.8	869	6	CA279117	CA279117 SCBFRT309
c1399	19	0.8	870	9	CR065595	CR065595 Reverse s
c1400	19	0.8	871	9	CL311713	CL311713 290998_LB
1401	19	0.8	873	9	CR015977	CR015977 Reverse s
c1402	19	0.8	873	9	CR242647	CR242647 Forward s
1403	19	0.8	877	8	CC378867	CC378867 PUHTX49TD
c1404	19	0.8	879	7	CV435383	CV435383 58928.1 S
c1405	19	0.8	881	9	CR248585	CR248585 Reverse s
c1406	19	0.8	884	4	BI663264	BI663264 603287307
1407	19	0.8	888	5	BU372222	BU372222 603812471
c1408	19	0.8	889	6	CA164571	CA164571 SCACRZ303
c1409	19	0.8	894	9	CR138136	CR138136 Forward s
1410	19	0.8	895	7	CO985868	CO985868 GM89015B1
c1411	19	0.8	902	9	CR047917	CR047917 Forward s
1412	19	0.8	907	5	BX342106	BX342106 BX342106
c1413	19	0.8	907	7	CK021524	CK021524 AGENCOURT
1414	19	0.8	907	8	CC433385	CC433385 PUHPK62TD
c1415	19	0.8	908	5	BU110316	BU110316 603127962
1416	19	0.8	909	2	BF100648	BF100648 601754181
c1417	19	0.8	912	9	CR269741	CR269741 Forward s
c1418	19	0.8	914	1	AV383794	AV383794 AV383794
c1419	19	0.8	915	7	CO019038	CO019038 EST815131
c1420	19	0.8	924	4	BI195155	BI195155 602944163
1421	19	0.8	924	9	CR041053	CR041053 Forward s
c1422	19	0.8	926	5	BX392121	BX392121 BX392121
c1423	19	0.8	927	2	BE421230	BE421230 HWM007.B0
c1424	19	0.8	927	8	BH136483	BH136483 ENTPC05TF
1425	19	0.8	928	9	CG064409	CG064409 PUIIO81TB
1426	19	0.8	930	8	CC381236	CC381236 PUHTO49TD
1427	19	0.8	933	9	CG191208	CG191208 PUJFE62TD
c1428	19	0.8	934	9	CL135068	CL135068 ISB1-105P
1429	19	0.8	935	9	CG062770	CG062770 PUJCK73TD
c1430	19	0.8	936	1	AL528153	AL528153 AL528153
c1431	19	0.8	936	5	BQ233428	BQ233428 AGENCOURT
1432	19	0.8	936	9	CC720286	CC720286 OGOBJ34TV
c1433	19	0.8	937	4	BG431828	BG431828 602498245

c1434	19	0.8	942	7	CN024707	CN024707 AGENCOURT
1435	19	0.8	944	5	BQ644298	BQ644298 AGENCOURT
1436	19	0.8	945	5	BQ920325	BQ920325 AGENCOURT
c1437	19	0.8	950	4	BG176642	BG176642 602313233
c1438	19	0.8	951	9	CG950145	CG950145 MBELC53TR
1439	19	0.8	956	3	CNS08HGB	BX012039 Single re
c1440	19	0.8	961	3	CNS08HGA	BX012038 Single re
1441	19	0.8	962	4	BM564748	BM564748 AGENCOURT
c1442	19	0.8	964	7	CO021452	CO021452 EST817545
1443	19	0.8	976	6	CB558602	CB558602 AGENCOURT
c1444	19	0.8	981	9	CNS03XK2	AL265115 Tetraodon
c1445	19	0.8	995	2	BE874561	BE874561 601489675
1446	19	0.8	999	6	BY703340	BY703340 BY703340
1447	19	0.8	1024	9	CC807659	CC807659 ZMMBBc051
c1448	19	0.8	1027	5	BU839991	BU839991 AGENCOURT
1449	19	0.8	1028	9	CG134064	CG134064 PUFWP09TB
c1450	19	0.8	1032	4	BM470515	BM470515 AGENCOURT
1451	19	0.8	1035	6	BY710380	BY710380 BY710380
1452	19	0.8	1041	8	CC208131	CC208131 CH261-101
c1453	19	0.8	1050	2	BF167041	BF167041 601774184
1454	19	0.8	1068	4	BM554996	BM554996 AGENCOURT
1455	19	0.8	1079	9	CNS05A0K	AL327917 Tetraodon
1456	19	0.8	1104	9	CL066126	CL066126 CH216-108
c1457	19	0.8	1105	8	BZ558839	BZ558839 pacs2-164
1458	19	0.8	1108	9	CL084072	CL084072 ISB1-2N8_
1459	19	0.8	1115	8	CC240393	CC240393 CH261-187
1460	19	0.8	1118	8	BZ695338	BZ695338 SP__Ba006
c1461	19	0.8	1119	9	CL026139	CL026139 CH216-22K
c1462	19	0.8	1120	1	AL535310	AL535310 AL535310
1463	19	0.8	1137	3	AK011093	AK011093 Mus muscu
1464	19	0.8	1145	3	AK010997	AK010997 Mus muscu
1465	19	0.8	1148	8	BZ566016	BZ566016 pacs2-164
1466	19	0.8	1156	7	CN642903	CN642903 ILLUMIGEN
1467	19	0.8	1166	9	AG391351	AG391351 Mus muscu
1468	19	0.8	1196	8	CC228428	CC228428 CH261-157
c1469	19	0.8	1206	8	CC274268	CC274268 CH261-20E
c1470	19	0.8	1208	8	B10713	B10713 F20L14-T7 I
c1471	19	0.8	1229	5	BQ938033	BQ938033 AGENCOURT
1472	19	0.8	1239	5	BQ073691	BQ073691 AGENCOURT
c1473	19	0.8	1268	3	CR729855	CR729855 Tetraodon
1474	19	0.8	1275	9	CL953223	CL953223 OsJRUA000
c1475	19	0.8	1280	3	CR731214	CR731214 Tetraodon
c1476	19	0.8	1285	3	CR692694	CR692694 Tetraodon
c1477	19	0.8	1316	9	CG755342	CG755342 P051-1-B0
c1478	19	0.8	1329	3	CR661548	CR661548 Tetraodon
1479	19	0.8	1333	9	AG170919	AG170919 Pan trogl
c1480	19	0.8	1337	3	CR731636	CR731636 Tetraodon
1481	19	0.8	1523	2	BE548217	BE548217 601074276
c1482	19	0.8	1778	6	CD385837	CD385837 AGENCOURT
c1483	19	0.8	1970	3	AK042731	AK042731 Mus muscu
c1484	19	0.8	2024	3	AK039504	AK039504 Mus muscu
1485	19	0.8	2086	9	AY420699	AY420699 Homo sapi
1486	19	0.8	2086	9	AY420701	AY420701 Mus muscu
c1487	19	0.8	2235	3	AK077792	AK077792 Mus muscu
1488	19	0.8	2355	3	AK002841	AK002841 Mus muscu
1489	19	0.8	2547	9	AY418202	AY418202 Mus muscu
c1490	19	0.8	2655	3	AK039095	AK039095 Mus muscu

1491	19	0.8	2773	3	AK082063	AK082063 Mus muscu
1492	19	0.8	3600	3	AK080619	AK080619 Mus muscu
1493	19	0.8	3694	3	AK032317	AK032317 Mus muscu
1494	19	0.8	4233	3	AK037707	AK037707 Mus muscu
c1495	18	0.8	57	8	AZ755655	AZ755655 ev02f07.x
1496	18	0.8	84	1	AA256701	AA256701 zr83h11.s
c1497	18	0.8	111	8	AZ241770	AZ241770 RPCI-23-8
1498	18	0.8	115	9	CL888966	CL888966 abf93c06.
c1499	18	0.8	136	1	AA780996	AA780996 ah32e01.s
1500	18	0.8	143	5	BQ511622	BQ511622 EST619037

ALIGNMENTS

RESULT 1
AY404343
LOCUS AY404343 1182 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY404343
VERSION AY404343.1 GI:39760320
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1182)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1182)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .1182
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1. .>1182
/locus_tag="HCM1859"
ORIGIN

Query Match 48.8%; Score 1131; DB 9; Length 1182;
Best Local Similarity 99.9%; Pred. No. 0;

```
  Matches 1181;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        458 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT 60

Qy        518 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTC 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTC 120

Qy        578 GGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTG 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTG 180

Qy        638 CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC 240

Qy        698 TGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTCACA 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTCACA 300

Qy        758 GAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC 360

Qy        818 TCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGC 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGC 420

Qy        878 TTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTT 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTT 480

Qy        938 GGGGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCG 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCG 540

Qy        998 GAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAG 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAG 600

Qy       1058 TGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGAC 1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGAC 660

Qy       1118 TGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGC 1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGC 720

Qy       1178 GGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTC 1237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTC 780

Qy       1238 TTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATT 1297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATT 840
```

```
Qy       1298 CAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGAC 1357
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGAC 900

Qy       1358 AAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGC 1417
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGC 960

Qy       1418 CCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCAC 1477
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCAC 1020

Qy       1478 CTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTG 1537
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1021 CTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTG 1080

Qy       1538 TTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCT 1597
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCT 1140

Qy       1598 GTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAA 1639
             |||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAA 1182
```

```
RESULT 2
CN396938
LOCUS       CN396938                759 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000417785787 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN396938
VERSION     CN396938.1  GI:47384533
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 759   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .759
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
```

/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

ORIGIN

Query Match 32.5%; Score 754; DB 7; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 754; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 65

Qy         61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 125

Qy        121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 185

Qy        181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 245

Qy        241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 305

Qy        301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 365

Qy        361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 425

Qy        421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 485

Qy        481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 545

Qy        541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 605

Qy        601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 665
```

```
Qy        661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 725

Qy        721 GTCTACATTTGACAACACCATCAAGGAACATTTC 754
              |||||||||||||||||||||||||||||||||
Db        726 GTCTACATTTGACAACACCATCAAGGAACATTTC 759


RESULT 3
BQ216829
LOCUS       BQ216829                879 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7594754 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6043558
            5', mRNA sequence.
ACCESSION   BQ216829
VERSION     BQ216829.1  GI:20398229
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 879)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13284  row: l  column: 23
            High quality sequence start: 17
            High quality sequence stop: 671.
FEATURES             Location/Qualifiers
     source          1. .879
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6043558"
                     /tissue_type="embryonal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_92"
                     /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 2.5 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             31.2%;  Score 725;  DB 5;  Length 879;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  775;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy        804 TGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 TGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTG 84

Qy        864 TTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACT 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACT 144

Qy        924 TCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAACA 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 TCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAACA 204

Qy        984 CCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAG 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 CCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAG 264

Qy       1044 GGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATG 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATG 324

Qy       1104 TGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGT 1163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGT 384

Qy       1164 TTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGG 1223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 TTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGG 444

Qy       1224 TGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGT 1283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 TGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGT 504

Qy       1284 TTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAAC 1343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 TTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAAC 564

Qy       1344 AAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCT 1403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCT 624

Qy       1404 CCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAG 1463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 CCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAG 684

Qy       1464 GGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGT 1523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 GGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGC 744

Qy       1524 TCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGG 1579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 TCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGG 800


RESULT 4
CD050395
LOCUS       CD050395                  916 bp    mRNA    linear   EST 09-MAY-2003
DEFINITION  AGENCOURT_13977999 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
```

```
ACCESSION   CD050395
VERSION     CD050395.1  GI:30487290
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 916)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jamie Thompson, University of WI
             cDNA Library Preparation: Gina Zastrow-Hayes
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDKM37  row: m  column: 04
            High quality sequence start: 12
            High quality sequence stop: 721.
FEATURES             Location/Qualifiers
     source          1. .916
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic trophoblasts, made from WA01 stem
                     cells"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_173"
                     /note="Vector: pDONR201; Site_1: attP2; Site_2: attP1;
                     LIBR_PRIMING - oligo dT; METHOD - full-length enriched;
                     LIBR PROVIDER - Bradfield"
ORIGIN

  Query Match             24.3%;  Score 563;  DB 6;  Length 916;
  Best Local Similarity   99.9%;  Pred. No. 4.2e-289;
  Matches  683;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 113

Qy         61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 173

Qy        121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 233

Qy        181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 293
```

```
Qy        241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 353

Qy        301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 413

Qy        361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 473

Qy        421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 533

Qy        481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 CTTCGACAT-GTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 592

Qy        541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 652

Qy        601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 712

Qy        661 GGGCCGAGTGAAGAATTTTCTGAT 684
              |||||||||||||||||||||||||
Db        713 GGGCCGAGTGAAGAATTTTCTGAT 736
```

```
RESULT 5
CN396939
LOCUS       CN396939                 510 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000599940872 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN396939
VERSION     CN396939.1  GI:47384534
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
```

```
            Email: rbrandenberger@geron.com
            Insert Length: 510   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .510
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cell, retinoic acid and
                     mitogen-treated hES cell line H7"
                     /clone_lib="GRN_PRENEU"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from hES cell line H7 (p29) maintained in feeder-free
                     conditions. Embryoid bodies were generated in the presence
                     of all-trans retinoic and mitogens."
ORIGIN

  Query Match             19.7%;  Score 457;  DB 7;  Length 510;
  Best Local Similarity   99.8%;  Pred. No. 2.3e-232;
  Matches  507;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1109 ATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTC 1168
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTC 62

Qy       1169 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 1228
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 122

Qy       1229 ATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGT 1288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGT 182

Qy       1289 GTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 1348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 242

Qy       1349 ATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCTCCCAC 1408
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 ATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCTCCCAC 302

Qy       1409 CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGC 1468
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGC 362

Qy       1469 GCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCGAC 1528
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        363 GCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGAC 422

Qy       1529 GTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTG 1588
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTG 482

Qy       1589 GGCATGGCTGTCTGGTGGCTGCGTGGGG 1616
             ||||||||||||||||||||||||||||
Db        483 GGCATGGCTGTCTGGTGGCTGCGTGGGG 510
```

RESULT 6
AI917116/c
LOCUS AI917116 430 bp mRNA linear EST 14-DEC-1999
DEFINITION ts52a02.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232170 3', mRNA sequence.
ACCESSION AI917116
VERSION AI917116.1 GI:5636971
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 430)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1614 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 420.
FEATURES Location/Qualifiers
source 1. .430
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2232170"
/tissue_type="renal cell tumor"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid8"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.2 kb. Life Technologies catalog #: 11524-014"
ORIGIN

Query Match 18.5%; Score 430; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 6.5e-218;
Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1887 AAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAG 1946
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 430 AAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAG 371

Qy 1947 CCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCC 2006
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 370 CCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCC 311

```
Qy       2007 TCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAA 2066
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 TCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAA 251

Qy       2067 CATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCT 2126
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCT 191

Qy       2127 CTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACA 2186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACA 131

Qy       2187 GGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAG 2246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 GGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAG 71

Qy       2247 GCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTC 2306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          70 GCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTC 11

Qy       2307 CCCAACCTCA 2316
             ||||||||||
Db          10 CCCAACCTCA 1
```

```
RESULT 7
AI580389/c
LOCUS       AI580389                 422 bp    mRNA    linear   EST 05-APR-1999
DEFINITION  tm42f08.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160807 3',
            mRNA sequence.
ACCESSION   AI580389
VERSION     AI580389.1  GI:4564765
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 386.
FEATURES             Location/Qualifiers
     source          1. .422
                     /organism="Homo sapiens"
```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2160807"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 18.2%; Score 422; DB 1; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-213;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1888 AGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGC 1947
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGC 363

Qy       1948 CTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCT 2007
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCT 303

Qy       2008 CCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAAC 2067
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAAC 243

Qy       2068 ATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTC 2127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTC 183

Qy       2128 TTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAG 2187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 TTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAG 123

Qy       2188 GTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGG 2247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGG 63

Qy       2248 CATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCC 2307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCC 3

Qy       2308 CC 2309
             ||
Db          2 CC 1
```

RESULT 8
CB158774
LOCUS CB158774 481 bp mRNA linear EST 29-JAN-2003

```
DEFINITION  K-EST0218183 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-14-D07
            5', mRNA sequence.
ACCESSION   CB158774
VERSION     CB158774.1  GI:28143912
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 481)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 14  row: D  column: 07
            High quality sequence stop: 481.
FEATURES             Location/Qualifiers
     source          1. .481
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L18POOL1n1-14-D07"
                     /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
                     /lab_host="Top10F'"
                     /clone_lib="L18POOL1n1"
                     /note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
                     Site_2: NotI; The library was contributed by the Soares
                     laboratory and it was constructed as described by Bonaldo,
                     M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
                     6(9): 791-806. RNA was prepared from harvested cell
                     culture."
ORIGIN

  Query Match             17.0%;  Score 395;  DB 6;  Length 481;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-199;
  Matches  445;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 95

Qy         61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 155

Qy        121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        156 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGATGCCATTATCTACT 215
```

```
Qy        181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 275

Qy        241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 335

Qy        301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 395

Qy        361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 455

Qy        421 GTTGCAGTGCAGTCATTTTTTAAATA 446
              |||||||||||||||||||||||||||
Db        456 GTTGCAGTGCAGTCATTTTTTAAATA 481
```

```
RESULT 9
AA633698/c
LOCUS       AA633698                439 bp    mRNA    linear   EST 09-MAR-1998
DEFINITION  ag87a11.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
            IMAGE:1141436 3', mRNA sequence.
ACCESSION   AA633698
VERSION     AA633698.1  GI:2556912
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1564   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 399.
FEATURES             Location/Qualifiers
     source          1. .439
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1141436"
```

/dev_stage="hNT neurons"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene hNT neuron (#937233)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Differentiated, post mitotic hNT neurons. Average insert
size: 1.5 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5'
GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTT 3'"
ORIGIN

Query Match 16.1%; Score 373; DB 1; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.2e-187;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1876 TTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCT 1935
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 TTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCT 380

Qy       1936 CAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGA 1995
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 CAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGA 320

Qy       1996 CTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTA 2055
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 CTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTA 260

Qy       2056 TCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTC 2115
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 TCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTC 200

Qy       2116 CCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGAC 2175
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 CCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGAC 140

Qy       2176 ACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCT 2235
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCT 80

Qy       2236 TGGCTGAGCAGGC 2248
             |||||||||||||
Db          79 TGGCTGAGCAGGC 67
```

RESULT 10
BI827790
LOCUS BI827790 901 bp mRNA linear EST 04-OCT-2001
DEFINITION 603075472F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5167360 5',
mRNA sequence.
ACCESSION BI827790
VERSION BI827790.1 GI:15939340
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 901)

```
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11415  row: p  column: 17
            High quality sequence stop: 418.
FEATURES             Location/Qualifiers
     source          1. .901
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5167360"
                     /tissue_type="medulla"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_119"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source normal medulla from
                     anonymous male age 27.  Library  is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.3 kb, insert size range
                     0.9-3 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 013. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             14.9%;  Score 345;  DB 4;  Length 901;
  Best Local Similarity   99.7%;  Pred. No. 2.3e-172;
  Matches  395;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 83

Qy       1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 143

Qy       2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 203

Qy       2101 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 263

Qy       2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 323
```

```
Qy       2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        324 CAGTGAGCTCCTTCTTGGCTGAGCAGGCTTGGAGACTGTAGGTTTCCAGATTTCCTGAAA 383

Qy       2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA 2316
             |||||||||||||||||||||||||||||||||||
Db        384 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA 419


RESULT 11
BX109306/c
LOCUS       BX109306                462 bp    mRNA    linear   EST 07-FEB-2003
DEFINITION  BX109306 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGp998E035522 ;
            IMAGE:2232170, mRNA sequence.
ACCESSION   BX109306
VERSION     BX109306.1  GI:27835717
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 462)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998E035522.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.
FEATURES             Location/Qualifiers
     source          1. .462
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998E035522 ; IMAGE:2232170"
                     /tissue_type="renal cell tumor"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid8"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.2 kb. Life Technologies catalog #:
                     11524-014"
ORIGIN
```

```
  Query Match             14.1%;  Score 328;  DB 5;  Length 462;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-163;
  Matches  448;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1869 CCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCAC 1928
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 CCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCAC 403

Qy       1929 TGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCAC 1988
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 TGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCAC 343

Qy       1989 ACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTA 2048
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 ACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTA 283

Qy       2049 CTATCTATCATGGAATAACATCC-AAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTT 2107
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        282 CTATCTATCATGGAATAACATCCAAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTT 223

Qy       2108 TTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAG 2167
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 TTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAG 163

Qy       2168 GGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAG 2227
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 GGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAG 103

Qy       2228 CTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAA 2287
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 CTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAA 43

Qy       2288 GTTTACAGCGTTATCTCTCCCCAACCTCA 2316
             |||||||||||||||||||||||||||||
Db          42 GTTTACAGCGTTATCTCTCCCCAACCTCA 14


RESULT 12
BP431975
LOCUS       BP431975                 360 bp    mRNA    linear   EST 09-SEP-2003
DEFINITION  BP431975 leukemia cell normalized cDNA library Homo sapiens cDNA
            clone LEU2245_30_D1, mRNA sequence.
ACCESSION   BP431975
VERSION     BP431975.1  GI:34554674
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 360)
  AUTHORS   Takagaki,K., Katsuma,S., Horio,T., Kaminishi,Y., Hada,Y.,
            Tanaka,T., Ohgi,T. and Yano,J.
  TITLE     cDNA microarray analysis of altered gene expression in
            Ara-C-treated leukemia cells
  JOURNAL   Biochem. Biophys. Res. Commun. 309 (2), 351-358 (2003)
  MEDLINE   22831100
```

```
   PUBMED   12951057
COMMENT     Contact: Kazuchika Takagaki
            Research Laboratories
            Nippon Shinyaku Co. Ltd.
            Sakura 3-14-1, Tsukuba, Ibaraki 305-0003, Japan
            Tel: 81-29-850-6242
            Fax: 81-29-850-6217
            Email: k.takagaki@nippon-shinyaku.co.jp.
FEATURES             Location/Qualifiers
     source          1. .360
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="LEU2245_30_D1"
                     /cell_type="leukemia cell"
                     /clone_lib="leukemia cell normalized cDNA library"
                     /note="mRNA expressed in leukemia cells (mixture of
                     CCRF-CEM, K562, HL-60, MOLT-4, or RPMI-8226)"
ORIGIN

  Query Match             13.1%;  Score 305;  DB 5;  Length 360;
  Best Local Similarity   99.7%;  Pred. No. 5.5e-151;
  Matches  355;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1783 CATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGC 1842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 CATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGC 64

Qy       1843 AGAAATCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGA 1902
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 AGAATTCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGA 124

Qy       1903 TTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTT 1962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 TTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTT 184

Qy       1963 CCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTA 2022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTA 244

Qy       2023 GTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACAC 2082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACAC 304

Qy       2083 CTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCA 2138
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCA 360


RESULT 13
AI654867/c
LOCUS       AI654867                1055 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wb65c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2310550 3',
            mRNA sequence.
ACCESSION   AI654867
VERSION     AI654867.1  GI:4738846
KEYWORDS    EST.
```

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1055)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 777   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 451.
FEATURES             Location/Qualifiers
     source          1. .1055
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2310550"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GC6"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match             12.7%;  Score 294;  DB 1;  Length 1055;
  Best Local Similarity   99.7%;  Pred. No. 4.8e-145;
  Matches  344;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1450 CGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCA 1509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCA 422

Qy       1510 TGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATG 1569
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATG 362

Qy       1570 GCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAA 1629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        361 GCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAA 302

Qy       1630 GGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCATTT 1689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCATTT 242

Qy       1690 CTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCCTG 1749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCCTG 182

Qy       1750 TTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCAC 1794
              |||||||||||||||||||||||||||||||||||||||||||
Db        181 TTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCAC 137


RESULT 14
R19994
LOCUS       R19994                   460 bp    mRNA    linear   EST 17-APR-1995
DEFINITION  yg38h02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone
            IMAGE:34999 5' similar to SP:UDBX_RABIT P36514
            UDP-GLUCURONOSYLTRANSFERASE MICROSOMAL ;, mRNA sequence.
ACCESSION   R19994
VERSION     R19994.1  GI:774628
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 3245
            High quality sequence stops: 345
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 3245   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 345.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:407351"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:34999"
```

/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain 1NIB"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

Query Match 12.5%; Score 290; DB 7; Length 460;
Best Local Similarity 100.0%; Pred. No. 6.1e-143;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1044 GGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATG 1103
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 GGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATG 132

Qy       1104 TGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGT 1163
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         133 TGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGT 192

Qy       1164 TTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGG 1223
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         193 TTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGG 252

Qy       1224 TGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGT 1283
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         253 TGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGT 312

Qy       1284 TTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTT 1333
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         313 TTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTT 362
```

RESULT 15
BF510946/c
LOCUS BF510946 363 bp mRNA linear EST 06-DEC-2000
DEFINITION UI-H-BI4-apo-g-12-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3088318 3', mRNA sequence.
ACCESSION BF510946
VERSION BF510946.1 GI:11594170
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 363)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3088318"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Sub8"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub8
                     is a subtracted library derived from NCI_CGAP_Sub5. The
                     NCI_CGAP_Sub8 library had 2.5 million recombinants. A
                     single-stranded DNA preparation of NCI_CGAP_Sub5 was used
                     as a tracer in a subtractive  hybridization with a driver
                     comprising: a pool of clones from  NCI_CGAP_Sub5 (IMAGE
                     clone Ids 2732833-2737415, 3068040-3069191; 25% of the
                     driver population), a pool of clones from NCI_CGAP_Sub4
                     (IMAGE clone Ids 2723592-2729326; 25% of the driver
                     population), NCI_CGAP_Sub6 (pool AIF-AJU, IMAGE Ids
                     2728969-2733190; 25% of the driver population), and
                     NCI_CGAP_Sub7 (IMAGE Ids 3069192-3072238,
                     3081864-3084550; 25% of the driver population).
                     Subtraction was performed as previously described
                     [Bonaldo, Lennon & Soares (1996): Normalization and
                     Subtraction: Two  Approaches To Facilitate Gene Discovery.
                     Genome Research 6, 791-806.
                     TAG_TISSUE=germ cell
                     TAG_LIB=NCI_CGAP_GC4
                     TAG_SEQ=AAATC"
ORIGIN

  Query Match             12.3%;  Score 286;  DB 2;  Length 363;
  Best Local Similarity   99.7%;  Pred. No. 8.3e-141;
  Matches  336;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1980 CCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTC 2039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 CCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTC 294

Qy       2040 CTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAG 2099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 CTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAG 234

Qy       2100 TTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGA 2159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 TTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGA 174
```

```
Qy       2160 GAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCC 2219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 GAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCC 114

Qy       2220 ACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAA 2279
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        113 ACAGTGAGCTCCTTCTCGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAA 54

Qy       2280 AAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA 2316
             |||||||||||||||||||||||||||||||||||||
Db         53 AAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCA 17
```

Search completed: March 25, 2005, 11:50:31
Job time : 6963 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 07:50:21 ; Search time 9713 Seconds
(without alignments)
11573.778 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 agggtcccttagccgggcgc.....tctctccccaacctcactaa 2320

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2320	100.0	2320	6	AX697213	AX697213 Sequence
2	2320	100.0	2320	9	AY358416	AY358416 Homo sapi
3	2162	93.2	2341	6	AX136141	AX136141 Sequence

	4	2162	93.2	2341	6	BD123523	BD123523 Secretory
	5	2162	93.2	2341	9	AK075383	AK075383 Homo sapi
	6	1957	84.4	2944	6	AX548037	AX548037 Sequence
	7	905	39.0	1836	6	CQ726650	CQ726650 Sequence
c	8	807	34.8	88948	2	AC008947	AC008947 Homo sapi
	9	807	34.8	179513	9	AC016612	AC016612 Homo sapi
	10	776	33.4	2263	6	AX958403	AX958403 Sequence
c	11	536	23.1	148069	2	AC025476	AC025476 Homo sapi
c	12	468	20.2	594	6	AX136632	AX136632 Sequence
c	13	468	20.2	594	6	BD123872	BD123872 Secretory
	14	422	18.2	125145	2	AC022136	AC022136 Homo sapi
	15	230	9.9	2426	6	AR541778	AR541778 Sequence
	16	164	7.1	102255	2	AC026735	AC026735 Homo sapi
	17	156	6.7	88948	2	AC008947	AC008947 Homo sapi
	18	139	6.0	770	6	AX136483	AX136483 Sequence
	19	139	6.0	770	6	BD123723	BD123723 Secretory
	20	68	2.9	1572	6	AX359923	AX359923 Sequence
	21	68	2.9	2082	6	AX359921	AX359921 Sequence
	22	68	2.9	2086	6	AX327327	AX327327 Sequence
	23	68	2.9	2759	9	BC068446	BC068446 Homo sapi
	24	68	2.9	2797	6	AX155211	AX155211 Sequence
	25	68	2.9	2823	6	AX714604	AX714604 Sequence
	26	68	2.9	2823	9	AK057066	AK057066 Homo sapi
	27	68	2.9	3108	9	BC035012	BC035012 Homo sapi
	28	68	2.9	5002	6	CQ842882	CQ842882 Sequence
	29	68	2.9	5002	9	AK125803	AK125803 Homo sapi
	30	68	2.9	105885	9	AC008860	AC008860 Homo sapi
	31	59	2.5	148069	2	AC025476	AC025476 Homo sapi
	32	52	2.2	1842	6	AX747286	AX747286 Sequence
	33	52	2.2	1842	9	AK091977	AK091977 Homo sapi
	34	47	2.0	291	6	CQ740738	CQ740738 Sequence
	35	45	1.9	45	6	AX697217	AX697217 Sequence
c	36	45	1.9	125145	2	AC022136	AC022136 Homo sapi
c	37	30	1.3	165304	9	AC112204	AC112204 Homo sapi
c	38	29	1.2	277	6	CQ350335	CQ350335 Sequence
c	39	29	1.2	507	6	CQ337751	CQ337751 Sequence
	40	26	1.1	2192	10	BC034837	BC034837 Mus muscu
	41	26	1.1	2196	10	BC022134	BC022134 Mus muscu
	42	26	1.1	2210	10	AK128903	AK128903 Mus muscu
	43	26	1.1	2212	6	AX155214	AX155214 Sequence
	44	26	1.1	2228	10	BC025940	BC025940 Mus muscu
	45	26	1.1	156499	2	AC132893	AC132893 Mus muscu
c	46	26	1.1	156499	2	AC132893	AC132893 Mus muscu
	47	26	1.1	170142	9	AP002383	AP002383 Homo sapi
	48	26	1.1	174742	2	AC016896	AC016896 Homo sapi
	49	26	1.1	195466	2	AC032024	AC032024 Homo sapi
	50	26	1.1	251769	2	AC117913	AC117913 Rattus no
c	51	24	1.0	24	6	AX155221	AX155221 Sequence
	52	24	1.0	24	6	AX697215	AX697215 Sequence
c	53	24	1.0	24	6	AX697216	AX697216 Sequence
c	54	23	1.0	23	6	AX697387	AX697387 Sequence
	55	23	1.0	846	6	AR551278	AR551278 Sequence
	56	23	1.0	185771	2	BX510940	BX510940 Danio rer
	57	23	1.0	197225	9	AC093835	AC093835 Homo sapi
c	58	22	0.9	582	6	AR383593	AR383593 Sequence
c	59	22	0.9	582	6	AR383617	AR383617 Sequence
c	60	22	0.9	1706	9	HSU79259	U79259 Human clone

c	61	22	0.9	1707	6	CQ717576	CQ717576 Sequence
c	62	22	0.9	1744	9	BC002677	BC002677 Homo sapi
c	63	22	0.9	1744	9	BC014394	BC014394 Homo sapi
c	64	22	0.9	2661	6	CQ842468	CQ842468 Sequence
c	65	22	0.9	2661	9	AK125431	AK125431 Homo sapi
c	66	22	0.9	6236	6	AX459735	AX459735 Sequence
c	67	22	0.9	125287	9	HS159A19	AL031729 Human DNA
	68	22	0.9	149146	2	AL583851	AL583851 Homo sapi
	69	22	0.9	163233	2	AC123388	AC123388 Rattus no
c	70	22	0.9	167454	2	BX284610	BX284610 Homo sapi
	71	22	0.9	175542	2	AC150062	AC150062 Gallus ga
	72	22	0.9	177909	2	AC031997	AC031997 Homo sapi
	73	22	0.9	201493	9	AL691520	AL691520 Human DNA
	74	22	0.9	213393	2	AL645475	AL645475 Homo sapi
c	75	22	0.9	223443	2	AC112801	AC112801 Rattus no
	76	22	0.9	227099	2	AC130756	AC130756 Rattus no
c	77	22	0.9	242883	2	AC112055	AC112055 Rattus no
c	78	22	0.9	252427	2	AC111287	AC111287 Rattus no
c	79	21	0.9	21	6	AX697386	AX697386 Sequence
	80	21	0.9	32260	10	MMU298076	AJ298076 Mus muscu
c	81	21	0.9	83549	9	AC004752	AC004752 Homo sapi
	82	21	0.9	90450	10	AL627226	AL627226 Mouse DNA
c	83	21	0.9	102807	2	AP000674	AP000674 Homo sapi
	84	21	0.9	104824	9	HS73H22	AL035699 Human DNA
c	85	21	0.9	110000	2	AC091341_6	Continuation (7 of
	86	21	0.9	110000	2	AC117310_0	AC117310 Rattus no
c	87	21	0.9	119419	2	AP000666	AP000666 Homo sapi
c	88	21	0.9	126392	2	AC018785	AC018785 Homo sapi
	89	21	0.9	128422	9	AL357139	AL357139 Human DNA
c	90	21	0.9	131556	2	AC132404	AC132404 Mus muscu
	91	21	0.9	131746	2	AC084842	AC084842 Homo sapi
c	92	21	0.9	139260	9	AC066587	AC066587 Homo sapi
	93	21	0.9	140073	9	CNS01DTO	AL132819 Human chr
c	94	21	0.9	159600	2	AC113296	AC113296 Mus muscu
c	95	21	0.9	160341	9	AL161629	AL161629 Human DNA
c	96	21	0.9	160644	2	AC143585	AC143585 Macaca mu
	97	21	0.9	163569	2	AC023293	AC023293 Homo sapi
	98	21	0.9	164784	2	AP001384	AP001384 Homo sapi
c	99	21	0.9	166065	2	AC149014	AC149014 Papio anu
c	100	21	0.9	166294	2	BX537330	BX537330 Danio rer
c	101	21	0.9	166649	9	AL353633	AL353633 Human DNA
c	102	21	0.9	167470	2	AC136060	AC136060 Rattus no
c	103	21	0.9	167573	10	AC121587	AC121587 Mus muscu
	104	21	0.9	168202	10	AC134826	AC134826 Mus muscu
	105	21	0.9	169978	9	AC017013	AC017013 Homo sapi
c	106	21	0.9	170138	5	BX569781	BX569781 Zebrafish
c	107	21	0.9	172382	2	AC149046	AC149046 Papio anu
c	108	21	0.9	172453	2	AC015889	AC015889 Homo sapi
c	109	21	0.9	172793	2	AC023659	AC023659 Homo sapi
	110	21	0.9	174949	2	AC111342	AC111342 Rattus no
c	111	21	0.9	176766	10	AC113329	AC113329 Mus muscu
	112	21	0.9	179528	9	AC026189	AC026189 Homo sapi
c	113	21	0.9	180081	10	AC122496	AC122496 Mus muscu
	114	21	0.9	181186	2	AC069264	AC069264 Homo sapi
	115	21	0.9	181460	10	AL672181	AL672181 Mouse DNA
	116	21	0.9	184039	9	CNS018OX	AL109767 Human chr
c	117	21	0.9	184509	2	AC113237	AC113237 Canis fam

c	118	21	0.9	188305	10	AC147559 AC147559 Mus muscu
c	119	21	0.9	189995	9	AC018822 AC018822 Homo sapi
	120	21	0.9	195873	10	AL805944 AL805944 Mouse DNA
c	121	21	0.9	198652	9	AC009303 AC009303 Homo sapi
c	122	21	0.9	199275	9	AC011401 AC011401 Homo sapi
	123	21	0.9	199814	9	AC023480 AC023480 Homo sapi
	124	21	0.9	200317	9	HS69B13 AL035698 Human DNA
c	125	21	0.9	200655	9	AC091825 AC091825 Homo sapi
	126	21	0.9	202052	2	AC084827 AC084827 Mus muscu
	127	21	0.9	202587	2	AC119862 AC119862 Mus muscu
c	128	21	0.9	205183	2	AC093355 AC093355 Mus muscu
c	129	21	0.9	207974	10	AL831771 AL831771 Mouse DNA
	130	21	0.9	211973	2	AP001163 AP001163 Homo sapi
c	131	21	0.9	221535	9	AP001359 AP001359 Homo sapi
c	132	21	0.9	222856	2	AC128437 AC128437 Rattus no
c	133	21	0.9	225611	2	AC149606 AC149606 Mus muscu
c	134	21	0.9	230525	2	AC096982 AC096982 Rattus no
	135	21	0.9	234360	2	AC118763 AC118763 Rattus no
	136	21	0.9	239559	2	AC095531 AC095531 Rattus no
c	137	21	0.9	242227	10	AC124120 AC124120 Mus muscu
	138	21	0.9	252520	2	AC131432 AC131432 Rattus no
	139	21	0.9	252625	2	AC130076 AC130076 Rattus no
c	140	21	0.9	253026	2	AC098084 AC098084 Rattus no
c	141	21	0.9	254828	2	AC111760 AC111760 Rattus no
c	142	21	0.9	261672	2	AC111815 AC111815 Rattus no
	143	21	0.9	263236	2	AC094070 AC094070 Rattus no
c	144	21	0.9	264264	2	AC094210 AC094210 Rattus no
c	145	21	0.9	270063	10	AC117635 AC117635 Mus muscu
	146	21	0.9	275392	2	AC095297 AC095297 Rattus no
c	147	21	0.9	279589	2	AC073768 AC073768 Mus muscu
	148	21	0.9	291856	2	AC119388 AC119388 Rattus no
	149	21	0.9	294316	2	AC131613 AC131613 Rattus no
c	150	21	0.9	323764	2	BX511194 BX511194 Danio rer
c	151	21	0.9	344000	1	TACID1 AL445063 Thermopla
	152	21	0.9	349391	1	BX572095 BX572095 Prochloro
	153	20	0.9	298	6	CQ741582 CQ741582 Sequence
	154	20	0.9	464	11	G60984 G60984 SHGC-84035
c	155	20	0.9	513	14	CHDNAMGG X89243 Canine herp
c	156	20	0.9	573	14	AY373026 AY373026 Bean yell
c	157	20	0.9	573	14	AY376313 AY376313 Bean yell
	158	20	0.9	582	11	G97497 G97497 S208P6362RD
	159	20	0.9	669	9	HSA338450 AJ338450 Homo sapi
	160	20	0.9	739	11	BV037877 BV037877 S212P6686
	161	20	0.9	1742	3	AB072589 AB072589 Bombyx mo
	162	20	0.9	2677	9	BC025385 BC025385 Homo sapi
	163	20	0.9	2870	5	BC084686 BC084686 Danio rer
	164	20	0.9	3673	8	ATPHYE X76610 A.thaliana
c	165	20	0.9	32538	3	CEZK829 Z73899 Caenorhabdi
	166	20	0.9	40873	2	CEH04I09 Z92848 Caenorhabdi
	167	20	0.9	41330	3	CBRG35F02 AC084556 Caenorhab
c	168	20	0.9	42141	3	CEY54G9A AL032648 Caenorhab
	169	20	0.9	47081	3	CEUNC22 X15423 Caenorhabdi
c	170	20	0.9	47417	2	AC100702 AC100702 Mus muscu
c	171	20	0.9	48022	9	AC116617 AC116617 Homo sapi
	172	20	0.9	54962	3	CELTWIMUSC L10351 Caenorhabdi
	173	20	0.9	55379	2	AC083988 AC083988 Homo sapi
c	174	20	0.9	57655	2	AC100690 AC100690 Mus muscu

c 175	20	0.9	58427	8	ATF15J5	AL110123 Arabidops
c 176	20	0.9	62708	2	AC097780_3	Continuation (4 of
c 177	20	0.9	63015	10	AL732310	AL732310 Mouse DNA
178	20	0.9	67061	9	HSDJ306F2	AL121573 Human DNA
c 179	20	0.9	68673	2	AC124071	AC124071 Homo sapi
180	20	0.9	69158	2	AC107955	AC107955 Homo sapi
c 181	20	0.9	69158	2	AC107955	AC107955 Homo sapi
c 182	20	0.9	80355	2	AC016505	AC016505 Homo sapi
c 183	20	0.9	81099	9	AC110770	AC110770 Homo sapi
184	20	0.9	84224	9	AL358978	AL358978 Human DNA
c 185	20	0.9	87849	3	AC084453	AC084453 Caenorhab
186	20	0.9	90775	2	AC074396	AC074396 Homo sapi
c 187	20	0.9	91822	9	AC122697	AC122697 Homo sapi
188	20	0.9	92439	2	AC101765	AC101765 Mus muscu
c 189	20	0.9	94529	6	AX695977	AX695977 Sequence
190	20	0.9	94977	2	AC139987	AC139987 Rattus no
191	20	0.9	96512	9	AC022539	AC022539 Homo sapi
c 192	20	0.9	99892	5	BX323581	BX323581 Zebrafish
193	20	0.9	104281	8	AC129092	AC129092 Medicago
c 194	20	0.9	106525	9	AC068641	AC068641 Homo sapi
c 195	20	0.9	106724	10	AF130357	AF130357 Mus muscu
c 196	20	0.9	107514	2	AC026404	AC026404 Homo sapi
197	20	0.9	109075	5	AY739095	AY739095 Takifugu
c 198	20	0.9	110000	2	AC106549_0	AC106549 Rattus no
c 199	20	0.9	110000	2	AC106549_1	Continuation (2 of
200	20	0.9	110000	2	AC119467_0	AC119467 Rattus no
c 201	20	0.9	110000	2	AC151831_1	Continuation (2 of
c 202	20	0.9	110000	2	AC151831_2	Continuation (3 of
203	20	0.9	110000	2	CR555291_3	Continuation (4 of
204	20	0.9	110000	2	AC073860_2	Continuation (3 of
c 205	20	0.9	112010	2	AC010302	AC010302 Homo sapi
c 206	20	0.9	112978	9	AC022139	AC022139 Homo sapi
c 207	20	0.9	114290	9	AL138814	AL138814 Human DNA
c 208	20	0.9	114873	10	AC124211	AC124211 Mus muscu
c 209	20	0.9	115293	9	AC127460	AC127460 Homo sapi
210	20	0.9	115372	9	AL359202	AL359202 Human DNA
c 211	20	0.9	115399	2	AP004322	AP004322 Oryza sat
212	20	0.9	116871	2	AL138738	AL138738 Homo sapi
213	20	0.9	118787	10	AL844486	AL844486 Mouse DNA
214	20	0.9	120492	9	AC092580	AC092580 Homo sapi
c 215	20	0.9	121720	8	AC021044	AC021044 Arabidops
216	20	0.9	125507	9	AL450336	AL450336 Human DNA
217	20	0.9	126360	2	AC117274	AC117274 Bos tauru
218	20	0.9	128739	8	AP004741	AP004741 Oryza sat
219	20	0.9	131757	9	AC004540	AC004540 Homo sapi
c 220	20	0.9	133225	9	AC108089	AC108089 Homo sapi
221	20	0.9	135473	10	AC102705	AC102705 Mus muscu
c 222	20	0.9	137302	4	AY386695	AY386695 Oryctolag
223	20	0.9	138121	9	AC025431	AC025431 Homo sapi
c 224	20	0.9	138173	2	AC151513	AC151513 Dasypus n
c 225	20	0.9	139446	4	AY386697	AY386697 Oryctolag
c 226	20	0.9	140023	2	AC151646	AC151646 Dasypus n
c 227	20	0.9	140385	9	HS20B11	AL031770 Human DNA
228	20	0.9	142837	2	AC113232	AC113232 Canis fam
229	20	0.9	142867	9	AC091184	AC091184 Homo sapi
c 230	20	0.9	143118	2	AC079348	AC079348 Homo sapi
c 231	20	0.9	144652	2	CR388085	CR388085 Danio rer

c	232	20	0.9	145383	2	AC116816	AC116816 Mus muscu
	233	20	0.9	145564	5	AL929247	AL929247 Zebrafish
	234	20	0.9	147724	8	AP003525	AP003525 Oryza sat
c	235	20	0.9	149902	2	AC110667	AC110667 Canis fam
	236	20	0.9	151595	5	AL954191	AL954191 Zebrafish
	237	20	0.9	153134	5	BX663506	BX663506 Zebrafish
c	238	20	0.9	154359	2	AC021718	AC021718 Homo sapi
c	239	20	0.9	154821	8	AP003709	AP003709 Oryza sat
c	240	20	0.9	154864	9	AC008070	AC008070 Homo sapi
c	241	20	0.9	155010	2	CR524821	CR524821 Danio rer
	242	20	0.9	155332	9	AC109581	AC109581 Homo sapi
	243	20	0.9	156857	2	BX537298	BX537298 Mus muscu
	244	20	0.9	158093	9	AL390123	AL390123 Human DNA
c	245	20	0.9	159620	9	AL354835	AL354835 Human DNA
	246	20	0.9	160513	2	AC113563	AC113563 Canis fam
c	247	20	0.9	161674	10	AL807394	AL807394 Mouse DNA
c	248	20	0.9	161891	2	AC141360	AC141360 Sus scrof
c	249	20	0.9	161892	2	AC123875	AC123875 Mus muscu
	250	20	0.9	163243	9	AL513304	AL513304 Human DNA
	251	20	0.9	163688	2	AC148274	AC148274 Macropus
c	252	20	0.9	163861	9	AL356772	AL356772 Human DNA
c	253	20	0.9	164642	2	AC096873	AC096873 Rattus no
	254	20	0.9	164706	9	AC068614	AC068614 Homo sapi
c	255	20	0.9	164711	9	BS000216	BS000216 Pan trogl
	256	20	0.9	165036	9	AC133010	AC133010 Homo sapi
c	257	20	0.9	166600	9	AL391121	AL391121 Human DNA
c	258	20	0.9	166698	2	AC025158	AC025158 Homo sapi
c	259	20	0.9	167120	10	AC110178	AC110178 Mus muscu
c	260	20	0.9	167281	2	AP001147	AP001147 Homo sapi
	261	20	0.9	167874	10	BX950219	BX950219 Mouse DNA
	262	20	0.9	168544	9	AL513307	AL513307 Human DNA
c	263	20	0.9	170028	2	AP002435	AP002435 Homo sapi
c	264	20	0.9	170118	9	AC012384	AC012384 Homo sapi
c	265	20	0.9	171474	2	AC135752	AC135752 Rattus no
c	266	20	0.9	171742	5	CR388178	CR388178 Zebrafish
	267	20	0.9	171791	2	CR847938	CR847938 Danio rer
c	268	20	0.9	171850	2	AC102284	AC102284 Mus muscu
c	269	20	0.9	172460	2	AC079798	AC079798 Homo sapi
	270	20	0.9	172902	2	AL358816	AL358816 Homo sapi
	271	20	0.9	173277	2	AC148175	AC148175 Mus muscu
c	272	20	0.9	173641	2	AC141089	AC141089 Rattus no
	273	20	0.9	174256	2	AC022572	AC022572 Homo sapi
c	274	20	0.9	174548	9	AP002342	AP002342 Homo sapi
c	275	20	0.9	174712	10	AL831725	AL831725 Mouse DNA
	276	20	0.9	176080	2	AC118314	AC118314 Rattus no
	277	20	0.9	176268	2	AL591001	AL591001 Homo sapi
c	278	20	0.9	176304	2	AC102182	AC102182 Mus muscu
c	279	20	0.9	176344	2	AC023117	AC023117 Homo sapi
	280	20	0.9	177879	2	AC087822	AC087822 Homo sapi
	281	20	0.9	179668	2	CR626936	CR626936 Danio rer
c	282	20	0.9	179686	2	AC023987	AC023987 Homo sapi
	283	20	0.9	180000	2	AC006394	AC006394 Homo sapi
c	284	20	0.9	180633	2	AC080056	AC080056 Homo sapi
c	285	20	0.9	180652	2	CR762436	CR762436 Danio rer
	286	20	0.9	182250	2	AC139988	AC139988 Rattus no
	287	20	0.9	182411	9	AC068044	AC068044 Homo sapi
c	288	20	0.9	183460	9	AL356753	AL356753 Human DNA

c	289	20	0.9	183905	2	CR847569 CR847569 Danio rer
c	290	20	0.9	184037	9	CNS01RIM AL163642 Human chr
	291	20	0.9	184583	2	AC079104 AC079104 Homo sapi
c	292	20	0.9	184660	2	BX323862 BX323862 Danio rer
	293	20	0.9	184794	2	AP000849 AP000849 Homo sapi
	294	20	0.9	185375	2	AC108789 AC108789 Mus muscu
c	295	20	0.9	186930	9	AP001604 AP001604 Homo sapi
	296	20	0.9	187614	2	AC115839 AC115839 Mus muscu
	297	20	0.9	188890	2	CR628370 CR628370 Danio rer
	298	20	0.9	188928	10	AC144630 AC144630 Mus muscu
c	299	20	0.9	189442	10	AC119382 AC119382 Rattus no
c	300	20	0.9	189616	10	AC124480 AC124480 Mus muscu
	301	20	0.9	191120	2	AC148124 AC148124 Otolemur
c	302	20	0.9	191448	2	AC124634 AC124634 Mus muscu
	303	20	0.9	191927	2	AC109884 AC109884 Rattus no
c	304	20	0.9	192042	9	AC079955 AC079955 Homo sapi
c	305	20	0.9	193483	9	AL356257 AL356257 Human DNA
	306	20	0.9	193960	2	AC018905 AC018905 Homo sapi
	307	20	0.9	194053	2	AC119434 AC119434 Mus muscu
	308	20	0.9	194104	10	AC124510 AC124510 Mus muscu
c	309	20	0.9	194143	8	ATCHRIV48 AL161548 Arabidops
c	310	20	0.9	194827	2	BX294106 BX294106 Danio rer
c	311	20	0.9	195449	10	AC133510 AC133510 Mus muscu
c	312	20	0.9	195466	2	AC032024 AC032024 Homo sapi
	313	20	0.9	195549	2	AC151860 AC151860 Bos tauru
	314	20	0.9	198197	2	BX322641 BX322641 Mus muscu
	315	20	0.9	198197	10	AC125035 AC125035 Mus muscu
	316	20	0.9	198831	10	AC122355 AC122355 Mus muscu
c	317	20	0.9	200153	2	AC116759 AC116759 Mus muscu
c	318	20	0.9	200856	5	BX248239 BX248239 Zebrafish
	319	20	0.9	201197	9	HS1091N2 AL590764 Homo sapi
c	320	20	0.9	204646	2	AC121130 AC121130 Mus muscu
	321	20	0.9	206291	2	AC069188 AC069188 Homo sapi
c	322	20	0.9	207818	2	AC137432 AC137432 Rattus no
	323	20	0.9	210915	2	AC116469 AC116469 Mus muscu
c	324	20	0.9	211094	5	BX005335 BX005335 Zebrafish
c	325	20	0.9	211178	10	AC139209 AC139209 Mus muscu
c	326	20	0.9	211743	2	AC136147 AC136147 Mus muscu
c	327	20	0.9	211799	2	AC138229 AC138229 Mus muscu
	328	20	0.9	212186	10	AC132237 AC132237 Mus muscu
c	329	20	0.9	212883	2	AC068832 AC068832 Homo sapi
	330	20	0.9	213153	2	AC129348 AC129348 Rattus no
c	331	20	0.9	213869	2	AC127959 AC127959 Rattus no
c	332	20	0.9	214756	2	AC119367 AC119367 Rattus no
	333	20	0.9	214868	2	AC139122 AC139122 Rattus no
c	334	20	0.9	216615	10	AC107850 AC107850 Mus muscu
c	335	20	0.9	219944	2	AC106194 AC106194 Rattus no
c	336	20	0.9	220558	2	AC096523 AC096523 Rattus no
	337	20	0.9	223337	10	AL928564 AL928564 Mouse DNA
	338	20	0.9	223367	9	AC018686 AC018686 Homo sapi
	339	20	0.9	224386	2	AC099090 AC099090 Rattus no
	340	20	0.9	224445	2	AC098492 AC098492 Rattus no
	341	20	0.9	225665	2	AC098177 AC098177 Rattus no
c	342	20	0.9	225803	2	AC123641 AC123641 Mus muscu
c	343	20	0.9	226433	2	AC109076 AC109076 Rattus no
c	344	20	0.9	226904	2	AC111606 AC111606 Rattus no
	345	20	0.9	227759	2	AC094147 AC094147 Rattus no

346	20	0.9	229425	2	AC126965	AC126965 Rattus no
c 347	20	0.9	230097	2	AC103195	AC103195 Rattus no
c 348	20	0.9	230765	2	AC140337	AC140337 Mus muscu
c 349	20	0.9	233527	2	AC128398	AC128398 Rattus no
c 350	20	0.9	233619	2	AC128426	AC128426 Rattus no
c 351	20	0.9	234771	2	AC105616	AC105616 Rattus no
352	20	0.9	235045	2	AC119588	AC119588 Rattus no
c 353	20	0.9	235363	10	AC022062	AC022062 Mus muscu
c 354	20	0.9	235977	2	AC111800	AC111800 Rattus no
c 355	20	0.9	236764	2	AC114057	AC114057 Rattus no
356	20	0.9	237258	2	AC124867	AC124867 Rattus no
357	20	0.9	237581	2	AC098349	AC098349 Rattus no
c 358	20	0.9	238427	2	AC113234	AC113234 Canis fam
359	20	0.9	238831	2	AC107158	AC107158 Rattus no
c 360	20	0.9	239657	2	AC096455	AC096455 Rattus no
c 361	20	0.9	240307	2	AC128067	AC128067 Rattus no
c 362	20	0.9	240597	2	AC094512	AC094512 Rattus no
363	20	0.9	241004	2	AC113922	AC113922 Rattus no
c 364	20	0.9	242036	2	AC126481	AC126481 Rattus no
c 365	20	0.9	242224	2	BX936445	BX936445 Danio rer
366	20	0.9	243863	2	AC137319	AC137319 Rattus no
c 367	20	0.9	246163	2	AC121406	AC121406 Rattus no
c 368	20	0.9	246387	2	AC109737	AC109737 Rattus no
369	20	0.9	248569	2	AC111477	AC111477 Rattus no
370	20	0.9	250492	2	AC137179	AC137179 Rattus no
c 371	20	0.9	250902	2	AC131965	AC131965 Rattus no
c 372	20	0.9	252779	2	AC114107	AC114107 Rattus no
c 373	20	0.9	253169	2	AC094461	AC094461 Rattus no
c 374	20	0.9	253613	2	AC122764	AC122764 Mus muscu
375	20	0.9	253877	2	AC106328	AC106328 Rattus no
376	20	0.9	254280	2	AC131372	AC131372 Rattus no
c 377	20	0.9	256058	2	AC111032	AC111032 Mus muscu
378	20	0.9	258795	2	AC123358	AC123358 Rattus no
379	20	0.9	259608	2	AC123181	AC123181 Rattus no
380	20	0.9	261792	2	AC114707	AC114707 Rattus no
c 381	20	0.9	262967	2	AC110392	AC110392 Rattus no
c 382	20	0.9	263371	2	AC098454	AC098454 Rattus no
383	20	0.9	265382	2	AC114439	AC114439 Rattus no
384	20	0.9	278103	2	AC115418	AC115418 Rattus no
c 385	20	0.9	287188	2	AC091344	AC091344 Rattus no
386	20	0.9	288383	2	AC109947	AC109947 Rattus no
c 387	20	0.9	310985	2	AC130582	AC130582 Rattus no
c 388	20	0.9	315291	2	AC134095	AC134095 Rattus no
c 389	20	0.9	340000	9	AP001699	AP001699 Homo sapi
c 390	20	0.9	340623	2	AC109956	AC109956 Rattus no
391	20	0.9	345588	2	AC119362	AC119362 Rattus no
392	20	0.9	348505	1	BX571870	BX571870 Photorhab
393	20	0.9	349505	2	AC130443	AC130443 Rattus no
c 394	20	0.9	349980	6	CQ870479	CQ870479 Sequence
c 395	20	0.9	349980	6	AX770909	AX770909 Sequence
c 396	19	0.8	165	8	AJ838560	AJ838560 Arabidops
397	19	0.8	282	11	HSU30330	U30330 Human seque
c 398	19	0.8	371	11	BV091192	BV091192 RPAMMSEQ0
399	19	0.8	376	11	G03350	G03350 human STS W
400	19	0.8	500	5	SSDYST2	AF137106 Sargocent
c 401	19	0.8	561	11	G77656	G77656 S210P6090RG
402	19	0.8	597	11	BV044600	BV044600 S212P6382

c	403	19	0.8	607	11	BV026830 BV026830 S209P6252
	404	19	0.8	665	4	AY356106 AY356106 Canis fam
c	405	19	0.8	674	6	CQ432519 CQ432519 Sequence
	406	19	0.8	719	6	AX067392 AX067392 Sequence
c	407	19	0.8	773	11	BV038537 BV038537 S212P6014
	408	19	0.8	834	4	AY355792 AY355792 Canis fam
	409	19	0.8	873	6	AX347498 AX347498 Sequence
	410	19	0.8	938	9	AK130214 AK130214 Homo sapi
	411	19	0.8	1144	8	BOBOPC5 X96408 B.oleracea
c	412	19	0.8	1218	6	AX570443 AX570443 Sequence
	413	19	0.8	1371	8	BOBOPC3 X96407 B.oleracea
c	414	19	0.8	1383	6	CQ741637 CQ741637 Sequence
	415	19	0.8	1441	8	BOBOCP4 X96409 B.oleracea
	416	19	0.8	1662	6	CQ742010 CQ742010 Sequence
c	417	19	0.8	1856	6	AX509814 AX509814 Sequence
	418	19	0.8	1933	9	AK130038 AK130038 Homo sapi
c	419	19	0.8	2000	6	AX508065 AX508065 Sequence
	420	19	0.8	2023	10	MMU10484 U10484 Mus musculu
	421	19	0.8	2024	9	HSA549090 AJ549090 Homo sapi
c	422	19	0.8	2103	8	AF105425 AF105425 Cynodon d
c	423	19	0.8	2206	6	BD209990 BD209990 Human tra
	424	19	0.8	2208	8	BOGBOCP4 X96410 B.oleracea
	425	19	0.8	2241	9	AY167927 AY167927 Homo sapi
	426	19	0.8	2263	10	BC052909 BC052909 Mus muscu
c	427	19	0.8	2309	6	BD157048 BD157048 Primer fo
c	428	19	0.8	2309	6	AX878147 AX878147 Sequence
c	429	19	0.8	2309	9	AK002085 AK002085 Homo sapi
c	430	19	0.8	2318	10	AF480164 AF480164 Mus muscu
c	431	19	0.8	2371	9	AF480163 AF480163 Homo sapi
	432	19	0.8	2406	9	HSA549088 AJ549088 Homo sapi
	433	19	0.8	2421	9	AY167926 AY167926 Homo sapi
	434	19	0.8	2424	6	AX528390 AX528390 Sequence
	435	19	0.8	2424	9	HSA549089 AJ549089 Homo sapi
	436	19	0.8	2538	6	CQ730160 CQ730160 Sequence
	437	19	0.8	2589	9	HSA272034 AJ272034 Homo sapi
	438	19	0.8	2589	9	HSA421783 AJ421783 Homo sapi
	439	19	0.8	2627	9	BC013947 BC013947 Homo sapi
c	440	19	0.8	2699	6	AR342388 AR342388 Sequence
c	441	19	0.8	2699	6	BD082295 BD082295 76 kDa, 3
	442	19	0.8	2714	10	BC060057 BC060057 Mus muscu
	443	19	0.8	2714	10	BC060243 BC060243 Mus muscu
	444	19	0.8	2724	6	AX347496 AX347496 Sequence
c	445	19	0.8	2798	6	AR342387 AR342387 Sequence
c	446	19	0.8	2798	6	BD082294 BD082294 76 kDa, 3
	447	19	0.8	2830	9	BC064390 BC064390 Homo sapi
c	448	19	0.8	2899	9	BC038424 BC038424 Homo sapi
	449	19	0.8	2954	6	CQ842138 CQ842138 Sequence
	450	19	0.8	2954	9	AK125168 AK125168 Homo sapi
	451	19	0.8	3195	10	AF190645 AF190645 Mus muscu
	452	19	0.8	3336	10	AF139923 AF139923 Mus muscu
	453	19	0.8	3550	6	BD190797 BD190797 Secreted
	454	19	0.8	3550	6	AX099520 AX099520 Sequence
c	455	19	0.8	3576	9	HSM806018 BX537516 Homo sapi
c	456	19	0.8	3810	9	HSM803390 AL832083 Homo sapi
c	457	19	0.8	4024	4	AF181119 AF181119 Sus scrof
	458	19	0.8	4068	3	AY280698 AY280698 Schistost
c	459	19	0.8	4127	3	AB032259 AB032259 Asterina

c	460	19	0.8	4158	9	HSM805995 BX537514 Homo sapi
	461	19	0.8	4283	9	AB020648 AB020648 Homo sapi
	462	19	0.8	4352	6	AR339064 AR339064 Sequence
	463	19	0.8	4597	10	RNO237670 AJ237670 Rattus no
	464	19	0.8	5205	2	AC018203 AC018203 Drosophil
	465	19	0.8	5947	3	PFSC04066 AL010241 Plasmodiu
	466	19	0.8	6875	8	AB028236 AB028236 Tricholom
c	467	19	0.8	8301	9	AC007456 AC007456 Homo sapi
	468	19	0.8	8388	9	HS17CTNS1 AF112441 Homo sapi
	469	19	0.8	9171	1	AE007469 AE007469 Streptoco
	470	19	0.8	9974	1	AE000629 AE000629 Helicobac
	471	19	0.8	10419	8	AB027513 AB027513 Tricholom
	472	19	0.8	10749	1	AE013819 AE013819 Yersinia
	473	19	0.8	10797	1	AE004396 AE004396 Vibrio ch
c	474	19	0.8	11004	1	AE001150 AE001150 Borrelia
	475	19	0.8	11258	1	AE000549 AE000549 Helicobac
	476	19	0.8	11447	1	AE000599 AE000599 Helicobac
	477	19	0.8	12507	1	AE011843 AE011843 Xanthomon
c	478	19	0.8	12973	2	AC013026 AC013026 Drosophil
	479	19	0.8	13206	2	AC014437 AC014437 Drosophil
c	480	19	0.8	14382	10	MMU50715 U50715 Mus musculu
	481	19	0.8	14506	1	AE005730 AE005730 Caulobact
	482	19	0.8	20543	8	AY028608 AY028608 Brassica
c	483	19	0.8	20549	2	AC068540 AC068540 Homo sapi
c	484	19	0.8	32551	3	CEC26D10 Z54327 Caenorhabdi
c	485	19	0.8	32768	6	CQ788980 CQ788980 Sequence
c	486	19	0.8	32768	6	AR218839 AR218839 Sequence
c	487	19	0.8	32768	6	BD003751 BD003751 Polynucle
	488	19	0.8	36298	3	U64842 U64842 Caenorhabdi
	489	19	0.8	36371	9	AC097643 AC097643 Homo sapi
	490	19	0.8	36428	9	AC110000 AC110000 Homo sapi
	491	19	0.8	37010	3	CBRG28M15 AC084544 Caenorhab
	492	19	0.8	37968	9	AC120115 AC120115 Homo sapi
c	493	19	0.8	39177	3	CEAC8 Z83097 Caenorhabdi
c	494	19	0.8	39329	9	AC004091 AC004091 Human Cos
c	495	19	0.8	39567	2	AC015562 AC015562 Homo sapi
c	496	19	0.8	39780	2	AC014011 AC014011 Drosophil
	497	19	0.8	41367	9	HSU163D10 Z68326 Human DNA s
c	498	19	0.8	41585	9	HSAC000374 AC000374 Human cos
c	499	19	0.8	42081	9	AC005494 AC005494 Homo sapi
c	500	19	0.8	42184	9	AC003068 AC003068 Human Cos
c	501	19	0.8	42296	8	AY459337 AY459337 Oryza sat
	502	19	0.8	42432	9	CR589904 CR589904 Human DNA
	503	19	0.8	43834	3	AF045643 AF045643 Caenorhab
	504	19	0.8	44008	9	AC097644 AC097644 Homo sapi
	505	19	0.8	44838	9	AC097642 AC097642 Homo sapi
c	506	19	0.8	44983	9	AL606913 AL606913 Human DNA
c	507	19	0.8	45976	9	AC091868 AC091868 Homo sapi
c	508	19	0.8	46530	2	BX293554_5 Continuation (6 of
	509	19	0.8	49297	9	AC063980 AC063980 Homo sapi
	510	19	0.8	50000	6	AR211704 AR211704 Sequence
	511	19	0.8	50913	7	AY129332 AY129332 Mycobacte
	512	19	0.8	53439	2	AC140621 AC140621 Macaca mu
c	513	19	0.8	55568	2	AC015850_3 Continuation (4 of
c	514	19	0.8	56168	2	AC101339 AC101339 Mus muscu
c	515	19	0.8	57571	2	AC018724_3 Continuation (4 of
	516	19	0.8	57671	2	AC117828 AC117828 Mus muscu

	517	19	0.8	58689	2	AC136343 AC136343 Homo sapi
	518	19	0.8	59777	3	AC084454 AC084454 Caenorhab
c	519	19	0.8	60406	9	AL590550 AL590550 Human DNA
c	520	19	0.8	60597	9	AC113611 AC113611 Homo sapi
c	521	19	0.8	62309	9	AC110495 AC110495 Homo sapi
	522	19	0.8	62677	2	AC100559 AC100559 Mus muscu
	523	19	0.8	62999	2	AC087594 AC087594 Homo sapi
	524	19	0.8	63238	2	AC137863 AC137863 Mus muscu
	525	19	0.8	64232	2	AC101806 AC101806 Mus muscu
	526	19	0.8	64601	9	AC009730 AC009730 Homo sapi
c	527	19	0.8	67220	2	AC022745 AC022745 Mus muscu
c	528	19	0.8	67468	2	AC139148 AC139148 Homo sapi
	529	19	0.8	67870	2	AC083787 AC083787 Homo sapi
c	530	19	0.8	67996	2	AC138912 AC138912 Homo sapi
	531	19	0.8	68222	9	AL391904 AL391904 Human DNA
c	532	19	0.8	69025	2	AC111171 AC111171 Homo sapi
c	533	19	0.8	69971	9	BX546457 BX546457 Human DNA
	534	19	0.8	70991	10	AY225417 AY225417 Mus muscu
c	535	19	0.8	71151	2	AC128128_3 Continuation (4 of
c	536	19	0.8	72351	2	AC100079 AC100079 Mus muscu
	537	19	0.8	73778	2	AC090743 AC090743 Homo sapi
c	538	19	0.8	73778	2	AC090743 AC090743 Homo sapi
	539	19	0.8	73842	2	AC025657 AC025657 Homo sapi
c	540	19	0.8	74135	2	AC141777 AC141777 Apis mell
	541	19	0.8	75803	8	AB016890 AB016890 Arabidops
c	542	19	0.8	76196	1	AY354515 AY354515 Streptomy
	543	19	0.8	76746	2	AC139032 AC139032 Homo sapi
	544	19	0.8	77127	9	AC104065 AC104065 Homo sapi
c	545	19	0.8	78346	12	AY350710 AY350710 Brassica
c	546	19	0.8	79355	2	AC021280 AC021280 Homo sapi
	547	19	0.8	79494	2	AC068837 AC068837 Homo sapi
	548	19	0.8	80817	9	AC146370 AC146370 Pan trogl
c	549	19	0.8	80828	5	AL672211 AL672211 Zebrafish
	550	19	0.8	81149	2	AC023338 AC023338 Homo sapi
c	551	19	0.8	82980	9	AL954237 AL954237 Pan trogl
	552	19	0.8	82998	2	AC022970 AC022970 Homo sapi
c	553	19	0.8	84348	5	BX649558 BX649558 Zebrafish
c	554	19	0.8	85297	9	AC079877 AC079877 Homo sapi
	555	19	0.8	85565	3	AC084423 AC084423 Caenorhab
c	556	19	0.8	85782	2	AC134656 AC134656 Rattus no
	557	19	0.8	88748	2	AC136733 AC136733 Mus muscu
c	558	19	0.8	88871	10	MMU58105 U58105 Mus musculu
	559	19	0.8	92245	9	AC073968 AC073968 Homo sapi
	560	19	0.8	92620	8	AB026636 AB026636 Arabidops
c	561	19	0.8	93287	9	AC023906 AC023906 Homo sapi
	562	19	0.8	93942	2	AC136851 AC136851 Rattus no
	563	19	0.8	94019	9	AL359971 AL359971 Human DNA
c	564	19	0.8	94255	9	AC003090 AC003090 Homo sapi
	565	19	0.8	95185	8	ATF6I7 AL049657 Arabidops
c	566	19	0.8	97118	2	AC096323_4 Continuation (5 of
	567	19	0.8	97473	9	AC127165 AC127165 Homo sapi
c	568	19	0.8	98119	2	AL357076 AL357076 Homo sapi
	569	19	0.8	98391	9	AC106733 AC106733 Homo sapi
c	570	19	0.8	98415	2	AC093587 AC093587 Homo sapi
	571	19	0.8	98461	8	ATT6H20 AL096859 Arabidops
c	572	19	0.8	99108	5	BX537146 BX537146 Zebrafish
c	573	19	0.8	99173	9	AL139800 AL139800 Human DNA

	574	19	0.8	99340	9	HSDJ770C6 AL109932 Human DNA
c	575	19	0.8	99886	9	HS598F2 AL021579 Human DNA
	576	19	0.8	100731	9	AC084030 AC084030 Homo sapi
	577	19	0.8	100909	2	AC134874 AC134874 Homo sapi
	578	19	0.8	101458	2	AP000680 AP000680 Homo sapi
c	579	19	0.8	101817	9	HS1216H12 AL008715 Human DNA
	580	19	0.8	101892	2	AC151425 AC151425 Medicago
c	581	19	0.8	102910	9	AB041512 AB041512 Homo sapi
	582	19	0.8	103135	10	AL954178 AL954178 Mouse DNA
	583	19	0.8	103574	9	HSAC002115 AC002115 Human DNA
	584	19	0.8	103577	9	AC009449 AC009449 Homo sapi
c	585	19	0.8	103933	10	AL805900 AL805900 Mouse DNA
	586	19	0.8	104776	9	AC022424 AC022424 Homo sapi
	587	19	0.8	105582	2	AC139065 AC139065 Homo sapi
c	588	19	0.8	105686	9	AC012072 AC012072 Homo sapi
	589	19	0.8	105935	5	BX548055 BX548055 Zebrafish
c	590	19	0.8	106429	2	AC132536_5 Continuation (6 of
c	591	19	0.8	106784	9	AF188029 AF188029 Homo sapi
	592	19	0.8	108271	9	AL445438 AL445438 Human DNA
c	593	19	0.8	108534	9	HS1240 9 AL021327 Human DNA
c	594	19	0.8	110000	1	AE016827_15 Continuation (16 o
c	595	19	0.8	110000	1	AE017354_27 Continuation (28 o
c	596	19	0.8	110000	1	BX908798_15 Continuation (16 o
c	597	19	0.8	110000	1	BX936398_24 Continuation (25 o
c	598	19	0.8	110000	1	CP000001_40 Continuation (41 o
c	599	19	0.8	110000	1	CP000013_4 Continuation (5 of
c	600	19	0.8	110000	1	CR628336_28 Continuation (29 o
	601	19	0.8	110000	2	AC095360_0 AC095360 Rattus no
c	602	19	0.8	110000	2	AC096323_3 Continuation (4 of
	603	19	0.8	110000	2	AC107170_0 AC107170 Rattus no
c	604	19	0.8	110000	2	AC108632_3 Continuation (4 of
c	605	19	0.8	110000	2	AC110502_3 Continuation (4 of
	606	19	0.8	110000	2	AC110675_3 Continuation (4 of
c	607	19	0.8	110000	2	AC112029_4 Continuation (5 of
	608	19	0.8	110000	2	AC126822_1 Continuation (2 of
	609	19	0.8	110000	2	AC142955_3 Continuation (4 of
	610	19	0.8	110000	2	AC151734_0 AC151734 Mus muscu
c	611	19	0.8	110000	2	AL390202_01 Continuation (2 of
c	612	19	0.8	110000	2	AL928982_2 Continuation (3 of
c	613	19	0.8	110000	2	AL928982_3 Continuation (4 of
	614	19	0.8	110000	8	CR382131_26 Continuation (27 o
	615	19	0.8	110000	8	CR382131_27 Continuation (28 o
	616	19	0.8	110983	2	AC110549 AC110549 Mus muscu
c	617	19	0.8	111074	9	AC007569 AC007569 Homo sapi
c	618	19	0.8	111372	2	AL353145 AL353145 Homo sapi
c	619	19	0.8	111731	2	BX323063 BX323063 Homo sapi
	620	19	0.8	112902	9	AC034211 AC034211 Homo sapi
	621	19	0.8	112997	2	AC151705 AC151705 Gallus ga
	622	19	0.8	113196	9	HSJ697K14 AL121829 Human DNA
	623	19	0.8	113798	10	AL591892 AL591892 Mouse DNA
	624	19	0.8	114411	9	AC112909 AC112909 Homo sapi
c	625	19	0.8	114434	9	AC093728 AC093728 Homo sapi
	626	19	0.8	115916	9	AC115220 AC115220 Homo sapi
c	627	19	0.8	116969	9	AL450423 AL450423 Human DNA
	628	19	0.8	117101	9	AC004061 AC004061 Homo sapi
c	629	19	0.8	119335	2	AC150947 AC150947 Bos tauru
	630	19	0.8	120612	9	AC108518 AC108518 Homo sapi

c	631	19	0.8	121483	4	BX323833 BX323833 Pig DNA s
	632	19	0.8	123556	9	HS507I15 Z98950 Human DNA s
c	633	19	0.8	123742	9	AC069431 AC069431 Homo sapi
	634	19	0.8	123766	2	AC151000 AC151000 Medicago
	635	19	0.8	125151	9	AC093821 AC093821 Homo sapi
c	636	19	0.8	125360	9	AC117406 AC117406 Homo sapi
c	637	19	0.8	125425	10	AC102845 AC102845 Mus muscu
c	638	19	0.8	125803	8	ATF22K18 AL035356 Arabidops
c	639	19	0.8	127061	2	AC118593 AC118593 Mus muscu
c	640	19	0.8	127431	9	AC027796 AC027796 Homo sapi
	641	19	0.8	127488	2	AC022095 AC022095 Homo sapi
	642	19	0.8	127576	5	AC144824 AC144824 Danio rer
	643	19	0.8	127686	2	AL591683 AL591683 Homo sapi
	644	19	0.8	127841	2	AC147714 AC147714 Medicago
c	645	19	0.8	128059	4	AY386694 AY386694 Oryctolag
c	646	19	0.8	128338	2	CR774177 CR774177 Danio rer
	647	19	0.8	128861	5	BX294435 BX294435 Zebrafish
	648	19	0.8	129231	9	AC092265 AC092265 Homo sapi
c	649	19	0.8	129461	2	CR677748 CR677748 Danio rer
c	650	19	0.8	129818	10	AC101831 AC101831 Mus muscu
	651	19	0.8	129831	10	AC147268 AC147268 Mus muscu
	652	19	0.8	130065	2	AC120329 AC120329 Rattus no
	653	19	0.8	130129	2	AC108083 AC108083 Homo sapi
	654	19	0.8	130494	2	AL139422 AL139422 Homo sapi
	655	19	0.8	131390	2	AC083986 AC083986 Homo sapi
c	656	19	0.8	131691	9	AC096765 AC096765 Homo sapi
	657	19	0.8	131769	9	AC104506 AC104506 Homo sapi
	658	19	0.8	132080	9	AC069368 AC069368 Homo sapi
c	659	19	0.8	133221	9	HS333A15 AL031429 Human DNA
	660	19	0.8	133242	8	AP003140 AP003140 Oryza sat
c	661	19	0.8	133519	10	AC140473 AC140473 Mus muscu
	662	19	0.8	133968	5	BX511174 BX511174 Zebrafish
	663	19	0.8	134597	2	CR391983 CR391983 Danio rer
	664	19	0.8	134972	2	CR388177 CR388177 Danio rer
c	665	19	0.8	134972	2	CR388177 CR388177 Danio rer
c	666	19	0.8	135063	10	AC099644 AC099644 Mus muscu
	667	19	0.8	135384	5	BX927227 BX927227 Zebrafish
	668	19	0.8	135453	2	AC118736 AC118736 Mus muscu
c	669	19	0.8	135800	2	AF523316 AF523316 Canis fam
	670	19	0.8	137562	2	AC151181 AC151181 Bos tauru
c	671	19	0.8	137705	10	AC140228 AC140228 Mus muscu
	672	19	0.8	137722	2	CR352240 CR352240 Danio rer
c	673	19	0.8	137830	2	AC024346 AC024346 Homo sapi
	674	19	0.8	137926	8	AP004867 AP004867 Oryza sat
	675	19	0.8	138634	10	AC140917 AC140917 Mus muscu
c	676	19	0.8	139058	2	AC145763 AC145763 Canis fam
c	677	19	0.8	139228	4	AC127467 AC127467 Atelerix
c	678	19	0.8	140023	4	AC093453 AC093453 Canis fam
	679	19	0.8	140856	9	AC002430 AC002430 Human BAC
	680	19	0.8	141466	2	AC110673 AC110673 Canis fam
	681	19	0.8	141548	2	AC109184 AC109184 Mus muscu
c	682	19	0.8	142010	8	AP003928 AP003928 Oryza sat
	683	19	0.8	143283	10	AC141877 AC141877 Mus muscu
	684	19	0.8	143503	5	BX677663 BX677663 Zebrafish
c	685	19	0.8	143682	9	AC108743 AC108743 Homo sapi
c	686	19	0.8	144301	9	AC010467 AC010467 Homo sapi
c	687	19	0.8	144382	10	AC147149 AC147149 Mus muscu

c 688	19	0.8	144658	9	AL138969	AL138969 Human DNA
c 689	19	0.8	144870	2	AC012135	AC012135 Homo sapi
690	19	0.8	145028	9	AC073875	AC073875 Homo sapi
691	19	0.8	145491	8	AP002883	AP002883 Oryza sat
692	19	0.8	145736	9	AL451139	AL451139 Human DNA
c 693	19	0.8	145962	2	CR352215	CR352215 Danio rer
694	19	0.8	145972	10	AC145608	AC145608 Mus muscu
695	19	0.8	145992	9	AC134919	AC134919 Homo sapi
696	19	0.8	146128	9	AC026358	AC026358 Homo sapi
697	19	0.8	146308	2	AC104751	AC104751 Mus muscu
698	19	0.8	146335	8	AP002521	AP002521 Oryza sat
699	19	0.8	146346	2	AC111120	AC111120 Mus muscu
c 700	19	0.8	146372	9	AL359174	AL359174 Human DNA
701	19	0.8	146383	2	AC016052	AC016052 Homo sapi
702	19	0.8	146410	9	AC006975	AC006975 Homo sapi
c 703	19	0.8	146442	10	AC099600	AC099600 Mus muscu
c 704	19	0.8	146885	2	BX957322	BX957322 Danio rer
c 705	19	0.8	147113	10	AC115033	AC115033 Mus muscu
706	19	0.8	147309	6	AX528392	AX528392 Sequence
707	19	0.8	148204	2	AC113238	AC113238 Felis cat
c 708	19	0.8	148656	9	AC005482	AC005482 Homo sapi
c 709	19	0.8	148737	9	AC026702	AC026702 Homo sapi
c 710	19	0.8	148801	9	AC100808	AC100808 Homo sapi
c 711	19	0.8	149298	2	AC119738	AC119738 Homo sapi
c 712	19	0.8	149320	2	AC126357	AC126357 Homo sapi
c 713	19	0.8	149579	10	AC147996	AC147996 Mus muscu
c 714	19	0.8	149712	2	AC140853	AC140853 Canis fam
c 715	19	0.8	150024	9	HS522P13	AL024509 Human DNA
c 716	19	0.8	150102	4	AY423389	AY423389 Canis fam
717	19	0.8	150150	8	AP002539	AP002539 Oryza sat
c 718	19	0.8	150186	10	AC140493	AC140493 Mus muscu
c 719	19	0.8	150573	9	AC097473	AC097473 Homo sapi
c 720	19	0.8	150641	5	AL935205	AL935205 Zebrafish
721	19	0.8	150751	9	AC092609	AC092609 Homo sapi
722	19	0.8	150772	2	AC131917	AC131917 Mus muscu
723	19	0.8	150957	8	OSJN00055	AL606628 Oryza sat
724	19	0.8	151152	6	CQ861610	CQ861610 Sequence
725	19	0.8	151152	9	HS454M7	AL022162 Human DNA
726	19	0.8	151163	9	HSA305P22	AL121673 Human DNA
727	19	0.8	151569	2	AC127473	AC127473 Canis fam
c 728	19	0.8	151628	2	AC016665	AC016665 Homo sapi
c 729	19	0.8	151655	9	AC012158	AC012158 Homo sapi
730	19	0.8	151874	2	AC011268	AC011268 Homo sapi
731	19	0.8	152341	9	AL137848	AL137848 Human DNA
732	19	0.8	152416	5	BX537336	BX537336 Zebrafish
733	19	0.8	152707	2	AC140215	AC140215 Mus muscu
c 734	19	0.8	152853	10	AC133082	AC133082 Mus muscu
735	19	0.8	152901	2	AC141346	AC141346 Rattus no
c 736	19	0.8	153001	10	AC147183	AC147183 Mus muscu
c 737	19	0.8	153021	10	AL663042	AL663042 Mouse DNA
738	19	0.8	153093	10	AC121939	AC121939 Mus muscu
c 739	19	0.8	153402	9	HS247E2	AL773569 Homo sapi
740	19	0.8	153746	9	AC108125	AC108125 Homo sapi
741	19	0.8	153866	2	AC137914	AC137914 Felis cat
c 742	19	0.8	153897	5	AL928656	AL928656 Zebrafish
743	19	0.8	154154	9	HS462O23	AL031431 Human DNA
744	19	0.8	154280	10	AC147622	AC147622 Mus muscu

c	745	19	0.8	154495	2	AC016646 AC016646 Homo sapi
c	746	19	0.8	154540	8	AP004632 AP004632 Oryza sat
	747	19	0.8	154648	10	AC145583 AC145583 Mus muscu
	748	19	0.8	154818	9	AL157711 AL157711 Human DNA
	749	19	0.8	154936	2	AC137907 AC137907 Canis fam
c	750	19	0.8	155179	10	AC132322 AC132322 Mus muscu
	751	19	0.8	155369	9	AL160058 AL160058 Human DNA
c	752	19	0.8	155490	2	AC015478 AC015478 Homo sapi
	753	19	0.8	155536	9	AC004112 AC004112 Homo sapi
c	754	19	0.8	155587	2	AC022053 AC022053 Homo sapi
c	755	19	0.8	155618	2	CR405702 CR405702 Danio rer
	756	19	0.8	155848	9	AC104996 AC104996 Homo sapi
c	757	19	0.8	156048	10	AC145562 AC145562 Mus muscu
	758	19	0.8	156577	10	AC140239 AC140239 Mus muscu
c	759	19	0.8	156656	9	AC021820 AC021820 Homo sapi
	760	19	0.8	156821	9	AC005691 AC005691 Homo sapi
	761	19	0.8	157042	2	CR759826 CR759826 Danio rer
	762	19	0.8	157216	9	AC087491 AC087491 Homo sapi
	763	19	0.8	157662	5	BX927072 BX927072 Zebrafish
	764	19	0.8	157783	2	AC119202 AC119202 Mus muscu
	765	19	0.8	157996	10	AC019026 AC019026 Mus muscu
	766	19	0.8	158018	5	AL953896 AL953896 Zebrafish
	767	19	0.8	158045	9	AC007432 AC007432 Homo sapi
c	768	19	0.8	158206	2	AC022661 AC022661 Homo sapi
c	769	19	0.8	158267	2	AC149770 AC149770 Bos tauru
	770	19	0.8	158387	2	AC095020 AC095020 Bos tauru
	771	19	0.8	158617	9	AC135972 AC135972 Homo sapi
	772	19	0.8	158678	10	AC108822 AC108822 Mus muscu
	773	19	0.8	158760	2	AC026098 AC026098 Homo sapi
	774	19	0.8	158872	10	AC133178 AC133178 Mus muscu
c	775	19	0.8	159320	9	AP006197 AP006197 Homo sapi
	776	19	0.8	159348	10	AC145373 AC145373 Mus muscu
c	777	19	0.8	159397	2	AC027040 AC027040 Homo sapi
	778	19	0.8	159419	5	AC144823 AC144823 Danio rer
	779	19	0.8	159605	2	AC120405 AC120405 Mus muscu
c	780	19	0.8	159927	9	AL353590 AL353590 Human DNA
	781	19	0.8	160138	9	AC008551 AC008551 Homo sapi
	782	19	0.8	160425	9	AL592153 AL592153 Human DNA
	783	19	0.8	160629	10	BX248578 BX248578 Mouse DNA
	784	19	0.8	160712	9	AC098799 AC098799 Homo sapi
	785	19	0.8	160781	2	AC128871 AC128871 Rattus no
	786	19	0.8	160796	10	AL592222 AL592222 Mouse DNA
	787	19	0.8	160891	9	AL512410 AL512410 Human DNA
c	788	19	0.8	161048	9	AC144510 AC144510 Pan trogl
	789	19	0.8	161070	2	AC149700 AC149700 Bos tauru
	790	19	0.8	161222	2	AC016037 AC016037 Homo sapi
	791	19	0.8	161640	2	AC119229 AC119229 Mus muscu
c	792	19	0.8	161647	9	AC079080 AC079080 Homo sapi
c	793	19	0.8	161830	9	AC110619 AC110619 Homo sapi
	794	19	0.8	162126	2	AC011784 AC011784 Homo sapi
c	795	19	0.8	162126	9	AL354711 AL354711 Human DNA
c	796	19	0.8	162132	10	AC147142 AC147142 Mus muscu
c	797	19	0.8	162345	2	AC147606 AC147606 Mus muscu
	798	19	0.8	162407	8	AP004121 AP004121 Oryza sat
c	799	19	0.8	162538	2	BX649414 BX649414 Homo sapi
	800	19	0.8	162743	10	AC144581 AC144581 Mus muscu
c	801	19	0.8	162932	2	AC018516 AC018516 Homo sapi

c	802	19	0.8	162935	10	AL359352 AL359352 Mouse DNA
	803	19	0.8	162981	10	AL844204 AL844204 Mouse DNA
c	804	19	0.8	162993	9	AC108105 AC108105 Homo sapi
c	805	19	0.8	163018	10	AC132254 AC132254 Mus muscu
c	806	19	0.8	163061	2	AC141982 AC141982 Rattus no
	807	19	0.8	163149	9	CNS01DSZ AL122057 Human chr
c	808	19	0.8	163183	3	AC009842 AC009842 Drosophil
c	809	19	0.8	163377	2	AC007897 AC007897 Homo sapi
	810	19	0.8	163419	5	BX323847 BX323847 Zebrafish
	811	19	0.8	163796	9	AC093725 AC093725 Homo sapi
c	812	19	0.8	163892	10	AC134567 AC134567 Mus muscu
	813	19	0.8	164612	10	AC124697 AC124697 Mus muscu
c	814	19	0.8	164702	6	AX706960 AX706960 Sequence
c	815	19	0.8	164702	6	AX707890 AX707890 Sequence
c	816	19	0.8	165151	2	BX936362 BX936362 Danio rer
c	817	19	0.8	165290	10	AC136638 AC136638 Mus muscu
c	818	19	0.8	165500	9	AP005139 AP005139 Homo sapi
c	819	19	0.8	165651	2	AC151393 AC151393 Atelerix
	820	19	0.8	165699	2	AP001802 AP001802 Homo sapi
	821	19	0.8	165777	10	BX004852 BX004852 Mouse DNA
c	822	19	0.8	165828	10	AC132283 AC132283 Mus muscu
c	823	19	0.8	165926	10	AC119876 AC119876 Mus muscu
c	824	19	0.8	165990	2	AC073509 AC073509 Homo sapi
c	825	19	0.8	166107	2	AC134334 AC134334 Mus muscu
	826	19	0.8	166138	9	AC099684 AC099684 Homo sapi
c	827	19	0.8	166183	9	AC073048 AC073048 Homo sapi
c	828	19	0.8	166257	9	AC012083 AC012083 Homo sapi
c	829	19	0.8	166306	9	AC022880 AC022880 Homo sapi
c	830	19	0.8	166451	2	AC025511 AC025511 Homo sapi
	831	19	0.8	166626	3	AC008318 AC008318 Drosophil
c	832	19	0.8	166651	4	AC087160 AC087160 Sus scrof
	833	19	0.8	166768	10	AC122796 AC122796 Mus muscu
	834	19	0.8	166777	2	AC106813 AC106813 Homo sapi
c	835	19	0.8	167022	9	AC010238 AC010238 Homo sapi
	836	19	0.8	167058	10	AL596183 AL596183 Mouse DNA
	837	19	0.8	167075	2	AC137909 AC137909 Canis fam
	838	19	0.8	167334	2	AC026034 AC026034 Homo sapi
	839	19	0.8	167734	9	AL157827 AL157827 Human DNA
c	840	19	0.8	167780	9	AL844892 AL844892 Human DNA
	841	19	0.8	167796	5	BX571826 BX571826 Zebrafish
	842	19	0.8	167878	9	AC096645 AC096645 Homo sapi
c	843	19	0.8	167940	2	CR356231 CR356231 Danio rer
c	844	19	0.8	168347	2	AC025336 AC025336 Homo sapi
	845	19	0.8	168569	10	AL671970 AL671970 Mouse DNA
	846	19	0.8	168601	10	AC132276 AC132276 Mus muscu
c	847	19	0.8	168608	2	AC090464 AC090464 Homo sapi
	848	19	0.8	168623	9	AC007649 AC007649 Homo sapi
	849	19	0.8	168624	9	AC092131 AC092131 Homo sapi
c	850	19	0.8	168668	10	AC138289 AC138289 Mus muscu
	851	19	0.8	168940	2	AC102307 AC102307 Mus muscu
	852	19	0.8	169046	5	AL928828 AL928828 Zebrafish
c	853	19	0.8	169393	9	AC146016 AC146016 Pan trogl
	854	19	0.8	169539	2	AC080095 AC080095 Homo sapi
	855	19	0.8	169628	5	BX322567 BX322567 Zebrafish
c	856	19	0.8	169686	2	BX465864 BX465864 Danio rer
	857	19	0.8	169892	2	CR589945 CR589945 Danio rer
c	858	19	0.8	170017	2	AC148158 AC148158 Zea mays

c	859	19	0.8	170027	2	AC110670 AC110670 Canis fam
c	860	19	0.8	170139	2	CR388179 CR388179 Danio rer
c	861	19	0.8	170425	2	AC024490 AC024490 Homo sapi
c	862	19	0.8	170455	2	AC025054 AC025054 Homo sapi
c	863	19	0.8	170479	10	AC147985 AC147985 Mus muscu
	864	19	0.8	170796	2	AC069416 AC069416 Homo sapi
	865	19	0.8	170842	9	AC007384 AC007384 Homo sapi
	866	19	0.8	170914	3	AC010843 AC010843 Drosophil
c	867	19	0.8	170914	3	AC010843 AC010843 Drosophil
	868	19	0.8	170988	10	AC121950 AC121950 Mus muscu
	869	19	0.8	171033	2	CR352213 CR352213 Danio rer
	870	19	0.8	171185	2	AP002424 AP002424 Homo sapi
	871	19	0.8	171188	2	AC005025 AC005025 Homo sapi
c	872	19	0.8	171266	2	BX323586 BX323586 Danio rer
c	873	19	0.8	171646	10	AC144851 AC144851 Mus muscu
c	874	19	0.8	171747	2	AC087678 AC087678 Homo sapi
c	875	19	0.8	171829	2	CR405711 CR405711 Danio rer
	876	19	0.8	171912	10	AC147150 AC147150 Mus muscu
	877	19	0.8	171982	2	AC120916 AC120916 Rattus no
	878	19	0.8	172134	2	AC138589 AC138589 Mus muscu
c	879	19	0.8	172246	9	AC024941 AC024941 Homo sapi
c	880	19	0.8	172327	2	AC012345 AC012345 Homo sapi
c	881	19	0.8	172371	2	AC092871 AC092871 Pan trogl
	882	19	0.8	172735	2	AC141005 AC141005 Rattus no
	883	19	0.8	172845	9	AL160053 AL160053 Human DNA
	884	19	0.8	172915	2	AC010160 AC010160 Homo sapi
	885	19	0.8	173003	10	AC125155 AC125155 Mus muscu
	886	19	0.8	173189	9	AC092323 AC092323 Homo sapi
c	887	19	0.8	173699	8	AP003416 AP003416 Oryza sat
c	888	19	0.8	173840	2	AC149585 AC149585 Mus muscu
	889	19	0.8	173882	9	HSAF001550 AF001550 Homo sapi
c	890	19	0.8	174021	9	AL358612 AL358612 Human DNA
c	891	19	0.8	174032	2	AC025904 AC025904 Homo sapi
	892	19	0.8	174033	2	AC021957 AC021957 Homo sapi
c	893	19	0.8	174116	2	AC026138 AC026138 Homo sapi
c	894	19	0.8	174152	10	AC132133 AC132133 Mus muscu
	895	19	0.8	174218	2	AC091071 AC091071 Oryza sat
	896	19	0.8	174269	2	AC132961 AC132961 Rattus no
c	897	19	0.8	174311	9	AP002788 AP002788 Homo sapi
	898	19	0.8	174591	2	AC140582 AC140582 Macaca mu
c	899	19	0.8	174617	2	AC023671 AC023671 Homo sapi
c	900	19	0.8	174633	2	AC126418 AC126418 Mus muscu
	901	19	0.8	174850	9	AL353745 AL353745 Human DNA
	902	19	0.8	174882	9	AC010585 AC010585 Homo sapi
	903	19	0.8	175294	10	AC145558 AC145558 Mus muscu
c	904	19	0.8	175317	9	AC104298 AC104298 Homo sapi
c	905	19	0.8	175406	10	AC131778 AC131778 Mus muscu
c	906	19	0.8	175421	2	AC140714 AC140714 Homo sapi
	907	19	0.8	175672	2	AC068691 AC068691 Homo sapi
c	908	19	0.8	175727	2	AC120798 AC120798 Mus muscu
	909	19	0.8	175747	2	BX571952 BX571952 Danio rer
c	910	19	0.8	175820	9	AL162378 AL162378 Human DNA
	911	19	0.8	175822	2	AC068402 AC068402 Homo sapi
c	912	19	0.8	175840	9	AC019306 AC019306 Homo sapi
c	913	19	0.8	175934	2	AC123868 AC123868 Mus muscu
c	914	19	0.8	176117	9	AC092352 AC092352 Homo sapi
	915	19	0.8	176153	9	AC006287 AC006287 Homo sapi

	916	19	0.8	176249	2	BX950226 BX950226 Danio rer
	917	19	0.8	176290	2	CR352241 CR352241 Homo sapi
c	918	19	0.8	176435	2	AC149874 AC149874 Xenopus t
c	919	19	0.8	176699	2	AC122967 AC122967 Rattus no
	920	19	0.8	176952	2	AC113805 AC113805 Rattus no
c	921	19	0.8	176965	2	AC148164 AC148164 Zea mays
c	922	19	0.8	177097	2	AP001569 AP001569 Homo sapi
	923	19	0.8	177223	10	AL663106 AL663106 Mouse DNA
c	924	19	0.8	177251	10	AC124565 AC124565 Mus muscu
c	925	19	0.8	177267	9	AC026116 AC026116 Homo sapi
c	926	19	0.8	177463	9	AP002853 AP002853 Homo sapi
	927	19	0.8	177852	2	AC034283 AC034283 Homo sapi
c	928	19	0.8	177969	10	AC122306 AC122306 Mus muscu
c	929	19	0.8	178004	2	AL590070 AL590070 Homo sapi
	930	19	0.8	178015	2	AC094993 AC094993 Rattus no
	931	19	0.8	178030	9	AC008406 AC008406 Homo sapi
c	932	19	0.8	178501	2	AC146738 AC146738 Otolemur
c	933	19	0.8	178528	10	AC131662 AC131662 Mus muscu
c	934	19	0.8	178560	2	AC134877 AC134877 Homo sapi
	935	19	0.8	178580	2	AC127948 AC127948 Rattus no
c	936	19	0.8	178780	9	AC121493 AC121493 Homo sapi
c	937	19	0.8	178981	2	AC149839 AC149839 Callithri
c	938	19	0.8	179110	9	AC011755 AC011755 Homo sapi
	939	19	0.8	179328	2	AC142429 AC142429 Rattus no
	940	19	0.8	179357	2	AC009625 AC009625 Homo sapi
c	941	19	0.8	179437	5	AL928892 AL928892 Zebrafish
c	942	19	0.8	179539	2	AC016369 AC016369 Homo sapi
c	943	19	0.8	179655	2	AC018940 AC018940 Homo sapi
c	944	19	0.8	179721	9	AC084356 AC084356 Homo sapi
	945	19	0.8	179726	9	AC007052 AC007052 Homo sapi
c	946	19	0.8	179755	9	AL603831 AL603831 Human DNA
	947	19	0.8	179840	2	AC068458 AC068458 Homo sapi
c	948	19	0.8	179941	10	AC142271 AC142271 Mus muscu
	949	19	0.8	180049	9	AC099558 AC099558 Homo sapi
	950	19	0.8	180520	2	AL714008 AL714008 Homo sapi
c	951	19	0.8	180530	10	AC136903 AC136903 Mus muscu
c	952	19	0.8	180563	2	AC034170 AC034170 Homo sapi
	953	19	0.8	180586	2	AC108912 AC108912 Mus muscu
c	954	19	0.8	180675	10	AC147991 AC147991 Mus muscu
c	955	19	0.8	180733	5	BX530027 BX530027 Zebrafish
	956	19	0.8	181034	2	AC135486 AC135486 Rattus no
c	957	19	0.8	181371	2	AC018893 AC018893 Homo sapi
c	958	19	0.8	181433	9	CNS00006 AL049775 Human chr
	959	19	0.8	181660	2	CR382295 CR382295 Danio rer
	960	19	0.8	181755	10	AC129289 AC129289 Mus muscu
c	961	19	0.8	181957	9	AC146382 AC146382 Pan trogl
c	962	19	0.8	182135	10	AC124184 AC124184 Mus muscu
c	963	19	0.8	182173	2	AC140974 AC140974 Papio ham
	964	19	0.8	182248	10	AL606915 AL606915 Mouse DNA
c	965	19	0.8	182256	9	AC005058 AC005058 Homo sapi
	966	19	0.8	182411	2	AC090408 AC090408 Homo sapi
	967	19	0.8	182534	10	AC101948 AC101948 Mus muscu
c	968	19	0.8	182586	2	AC053505 AC053505 Homo sapi
c	969	19	0.8	182741	2	AC112855 AC112855 Rattus no
c	970	19	0.8	182774	5	BX284646 BX284646 Zebrafish
	971	19	0.8	182798	2	AC025394 AC025394 Homo sapi
	972	19	0.8	182857	2	AC147219 AC147219 Mus muscu

c 973	19	0.8	182960	9	CNS01RHW	AL162551 Human chr
974	19	0.8	183093	9	AC138688	AC138688 Homo sapi
975	19	0.8	183121	2	AC093417	AC093417 Homo sapi
c 976	19	0.8	183133	10	AC101851	AC101851 Mus muscu
c 977	19	0.8	183315	10	AC140383	AC140383 Mus muscu
c 978	19	0.8	183707	10	AC124384	AC124384 Mus muscu
979	19	0.8	183894	9	AC040970	AC040970 Homo sapi
980	19	0.8	183901	2	AL356425	AL356425 Homo sapi
c 981	19	0.8	183987	10	AC145344	AC145344 Mus muscu
c 982	19	0.8	184490	2	AC123734	AC123734 Mus muscu
983	19	0.8	184663	2	AC012113	AC012113 Homo sapi
984	19	0.8	184769	9	AC016583	AC016583 Homo sapi
985	19	0.8	184822	2	AC118743	AC118743 Mus muscu
c 986	19	0.8	184966	2	AC146675	AC146675 Callithri
c 987	19	0.8	185095	8	AP003436	AP003436 Oryza sat
c 988	19	0.8	185174	9	AC073091	AC073091 Homo sapi
c 989	19	0.8	185417	9	AC012313	AC012313 Homo sapi
990	19	0.8	185481	2	AC091088	AC091088 Oryza sat
991	19	0.8	185573	2	AC010994	AC010994 Drosophil
c 992	19	0.8	185621	2	AC036195	AC036195 Homo sapi
c 993	19	0.8	185945	2	CR293528	CR293528 Danio rer
c 994	19	0.8	186078	9	AC037482	AC037482 Homo sapi
c 995	19	0.8	186278	9	AL928717	AL928717 Human DNA
996	19	0.8	186673	2	AL590713	AL590713 Homo sapi
997	19	0.8	187023	2	AC006882	AC006882 Caenorhab
998	19	0.8	187032	10	AC147372	AC147372 Mus muscu
c 999	19	0.8	187084	9	AC010269	AC010269 Homo sapi
c1000	19	0.8	187316	9	AL139340	AL139340 Human DNA
c1001	19	0.8	187367	2	AC099751	AC099751 Sus scrof
c1002	19	0.8	187490	2	AL691495	AL691495 Homo sapi
1003	19	0.8	187691	5	BX324194	BX324194 Zebrafish
1004	19	0.8	187738	10	AL845547	AL845547 Mouse DNA
c1005	19	0.8	187948	2	BX005227	BX005227 Danio rer
c1006	19	0.8	187960	9	AP000866	AP000866 Homo sapi
c1007	19	0.8	188285	9	AL135842	AL135842 Human DNA
c1008	19	0.8	188322	2	AC134541	AC134541 Mus muscu
1009	19	0.8	188330	2	AC139710	AC139710 Canis fam
1010	19	0.8	188333	9	AC146143	AC146143 Pan trogl
1011	19	0.8	188435	10	AC100263	AC100263 Mus muscu
c1012	19	0.8	188548	9	AC008661	AC008661 Homo sapi
c1013	19	0.8	188724	10	AC142113	AC142113 Mus muscu
1014	19	0.8	188844	2	AC127475	AC127475 Canis fam
1015	19	0.8	188895	5	BX004834	BX004834 Zebrafish
1016	19	0.8	188945	2	AC093697	AC093697 Homo sapi
1017	19	0.8	188951	2	AC126762	AC126762 Homo sapi
1018	19	0.8	189160	2	AC080074	AC080074 Homo sapi
1019	19	0.8	189272	2	AC119503	AC119503 Rattus no
c1020	19	0.8	189371	2	AC090230	AC090230 Homo sapi
1021	19	0.8	189490	10	AC136975	AC136975 Mus muscu
1022	19	0.8	189507	10	AC132441	AC132441 Mus muscu
1023	19	0.8	189728	10	AC140223	AC140223 Mus muscu
1024	19	0.8	189770	9	AC147329	AC147329 Pan trogl
1025	19	0.8	189814	9	AC145866	AC145866 Pan trogl
c1026	19	0.8	189822	9	AC092722	AC092722 Homo sapi
c1027	19	0.8	189828	2	AC069321	AC069321 Homo sapi
c1028	19	0.8	189903	2	AC012542	AC012542 Homo sapi
c1029	19	0.8	190024	9	AC122714	AC122714 Homo sapi

1030	19	0.8	190437	10	AC098724	AC098724 Mus muscu
c1031	19	0.8	190627	10	AL671982	AL671982 Mouse DNA
c1032	19	0.8	190648	9	CNS01DXI	AL139317 Human chr
1033	19	0.8	190649	2	BX663608	BX663608 Danio rer
1034	19	0.8	191121	2	AC083952	AC083952 Homo sapi
c1035	19	0.8	191191	9	AC000119	AC000119 Homo sapi
1036	19	0.8	191218	8	OSJN00171	AL662974 Oryza sat
c1037	19	0.8	191453	5	BX510648	BX510648 Zebrafish
c1038	19	0.8	191602	2	AC068920	AC068920 Homo sapi
1039	19	0.8	191613	10	AC132408	AC132408 Mus muscu
c1040	19	0.8	191665	9	AC027627	AC027627 Homo sapi
c1041	19	0.8	191856	9	AL355980	AL355980 Human DNA
1042	19	0.8	191942	9	AC079951	AC079951 Homo sapi
1043	19	0.8	192016	10	AC099582	AC099582 Mus muscu
c1044	19	0.8	192273	2	AC137982	AC137982 Mus muscu
c1045	19	0.8	192338	2	AC022221	AC022221 Homo sapi
1046	19	0.8	192584	10	AC131080	AC131080 Mus muscu
1047	19	0.8	192658	2	AC132225	AC132225 Mus muscu
1048	19	0.8	193001	2	AC151369	AC151369 Aotus nan
1049	19	0.8	193064	2	AC124333	AC124333 Mus muscu
1050	19	0.8	193153	2	AC141895	AC141895 Mus muscu
1051	19	0.8	193167	2	AC117938	AC117938 Canis fam
c1052	19	0.8	193279	9	AC009466	AC009466 Homo sapi
c1053	19	0.8	193526	3	AC010993	AC010993 Drosophil
c1054	19	0.8	193549	9	AC087286	AC087286 Homo sapi
1055	19	0.8	193811	10	AC134827	AC134827 Mus muscu
c1056	19	0.8	193944	4	AC147679	AC147679 Canis Fam
1057	19	0.8	193963	9	AC007336	AC007336 Homo sapi
1058	19	0.8	194048	2	AC147652	AC147652 Pan trogl
c1059	19	0.8	194065	10	AL772179	AL772179 Mouse DNA
c1060	19	0.8	194109	10	AC121819	AC121819 Mus muscu
c1061	19	0.8	194224	5	BX465842	BX465842 Zebrafish
1062	19	0.8	194301	2	AC103772	AC103772 Homo sapi
1063	19	0.8	194335	10	AC144934	AC144934 Mus muscu
c1064	19	0.8	194615	2	AC024190	AC024190 Homo sapi
1065	19	0.8	194631	2	BX936384	BX936384 Danio rer
1066	19	0.8	194845	2	AC123885	AC123885 Mus muscu
c1067	19	0.8	194994	2	AC020609	AC020609 Homo sapi
c1068	19	0.8	195156	2	AC019034	AC019034 Homo sapi
c1069	19	0.8	195333	2	AC134255	AC134255 Mus muscu
1070	19	0.8	195413	10	AL671881	AL671881 Mouse DNA
1071	19	0.8	195444	2	AC025424	AC025424 Mus muscu
1072	19	0.8	195480	2	CR847999	CR847999 Danio rer
c1073	19	0.8	195488	2	CR753885	CR753885 Danio rer
1074	19	0.8	195858	2	AC023879	AC023879 Homo sapi
c1075	19	0.8	195950	9	AC012003	AC012003 Homo sapi
1076	19	0.8	195981	2	AC112959	AC112959 Mus muscu
1077	19	0.8	195992	10	AC103618	AC103618 Mus muscu
1078	19	0.8	196099	10	AC147113	AC147113 Mus muscu
1079	19	0.8	196361	2	AC123351	AC123351 Rattus no
c1080	19	0.8	196372	10	AL929100	AL929100 Mouse DNA
1081	19	0.8	196501	9	AC005908	AC005908 Homo sapi
c1082	19	0.8	196712	10	AC137902	AC137902 Mus muscu
1083	19	0.8	196734	2	AC010640	AC010640 Homo sapi
c1084	19	0.8	196869	2	AC087535	AC087535 Homo sapi
1085	19	0.8	197070	8	ATCHRIV62	AL161562 Arabidops
1086	19	0.8	197164	9	AC064865	AC064865 Homo sapi

c1087	19	0.8	197281	2	CR762408	CR762408 Danio rer
1088	19	0.8	197330	2	AL928858	AL928858 Danio rer
1089	19	0.8	197519	2	AC145553	AC145553 Mus muscu
c1090	19	0.8	197582	2	AC151934	AC151934 Callithri
1091	19	0.8	197602	10	AC147252	AC147252 Mus muscu
1092	19	0.8	197605	2	AC026905	AC026905 Homo sapi
1093	19	0.8	197630	9	AC011676	AC011676 Homo sapi
1094	19	0.8	197652	9	AC012074	AC012074 Homo sapi
c1095	19	0.8	197946	10	AC098722	AC098722 Mus muscu
1096	19	0.8	197949	10	AC122204	AC122204 Mus muscu
c1097	19	0.8	197978	10	AC114821	AC114821 Mus muscu
c1098	19	0.8	198237	2	AC026299	AC026299 Homo sapi
1099	19	0.8	198242	10	AC116489	AC116489 Mus muscu
1100	19	0.8	198244	2	CR381546	CR381546 Danio rer
1101	19	0.8	198470	9	AC046170	AC046170 Homo sapi
c1102	19	0.8	198644	9	AL590964	AL590964 Human DNA
1103	19	0.8	198935	9	AC034268	AC034268 Homo sapi
c1104	19	0.8	198942	9	AC008517	AC008517 Homo sapi
c1105	19	0.8	198991	2	AC102227	AC102227 Mus muscu
c1106	19	0.8	199024	2	AC150721	AC150721 Callithri
1107	19	0.8	199702	2	AC087178	AC087178 Homo sapi
1108	19	0.8	199733	10	AC144647	AC144647 Mus muscu
c1109	19	0.8	199848	10	AL512647	AL512647 Mouse DNA
1110	19	0.8	199883	2	AC073736	AC073736 Mus muscu
c1111	19	0.8	199916	3	AC008099	AC008099 Drosophil
1112	19	0.8	200237	9	AF168787	AF168787 Homo sapi
c1113	19	0.8	200278	9	AC092797	AC092797 Homo sapi
1114	19	0.8	200420	9	AC138645	AC138645 Homo sapi
c1115	19	0.8	200774	2	AP001592	AP001592 Homo sapi
1116	19	0.8	200840	9	AL158072	AL158072 Human DNA
c1117	19	0.8	201139	10	AC122865	AC122865 Mus muscu
1118	19	0.8	201279	9	AC090133	AC090133 Homo sapi
1119	19	0.8	201376	2	AC112449	AC112449 Rattus no
c1120	19	0.8	201418	2	AC144493	AC144493 Bos tauru
c1121	19	0.8	201611	2	AC021185	AC021185 Homo sapi
c1122	19	0.8	201757	10	AC061963	AC061963 Mus muscu
1123	19	0.8	201917	2	AC108015	AC108015 Homo sapi
c1124	19	0.8	201964	10	MMMHC29N7	AF030001 Mus muscu
c1125	19	0.8	201986	10	AC006289	AC006289 Mus muscu
1126	19	0.8	202083	2	AC023833	AC023833 Mus muscu
1127	19	0.8	202338	10	AC147107	AC147107 Mus muscu
1128	19	0.8	202442	2	AC110203	AC110203 Mus muscu
1129	19	0.8	202600	2	AC151374	AC151374 Callithri
1130	19	0.8	202609	2	AC102911	AC102911 Mus muscu
1131	19	0.8	202772	2	CR384110	CR384110 Danio rer
1132	19	0.8	202955	9	AL356378	AL356378 Human DNA
c1133	19	0.8	203169	2	BX571855	BX571855 Danio rer
1134	19	0.8	203412	2	AC107270	AC107270 Rattus no
c1135	19	0.8	203427	2	AC111331	AC111331 Rattus no
1136	19	0.8	203486	10	AC131733	AC131733 Mus muscu
1137	19	0.8	203718	9	AC009486	AC009486 Homo sapi
c1138	19	0.8	203810	10	AC132612	AC132612 Mus muscu
1139	19	0.8	203838	2	AC026840	AC026840 Homo sapi
1140	19	0.8	203944	10	AC145292	AC145292 Mus muscu
c1141	19	0.8	204044	2	AC146926	AC146926 Callithri
c1142	19	0.8	204198	2	BX470261	BX470261 Danio rer
c1143	19	0.8	204724	10	AC131912	AC131912 Mus muscu

c1144	19	0.8	204944	2	BX537255	BX537255 Danio rer
c1145	19	0.8	204950	10	AC083817	AC083817 Mus muscu
1146	19	0.8	205004	9	AC090132	AC090132 Homo sapi
1147	19	0.8	205029	2	AC118189	AC118189 Rattus no
1148	19	0.8	205044	2	AC024453	AC024453 Homo sapi
c1149	19	0.8	205222	10	AC123534	AC123534 Mus muscu
c1150	19	0.8	205572	2	AC055724	AC055724 Homo sapi
1151	19	0.8	205816	10	AC113201	AC113201 Mus muscu
c1152	19	0.8	205859	2	AC099702	AC099702 Mus muscu
c1153	19	0.8	205903	9	AP000901	AP000901 Homo sapi
c1154	19	0.8	205993	2	AC119212	AC119212 Mus muscu
1155	19	0.8	206021	9	AC012065	AC012065 Homo sapi
c1156	19	0.8	206023	2	AC146657	AC146657 Otolemur
c1157	19	0.8	206187	2	AC069139	AC069139 Homo sapi
c1158	19	0.8	206494	10	AC138766	AC138766 Mus muscu
c1159	19	0.8	206537	9	AC099777	AC099777 Homo sapi
1160	19	0.8	206618	9	AF195953	AF195953 Homo sapi
c1161	19	0.8	206630	2	AC150604	AC150604 Callithri
c1162	19	0.8	206783	10	AC139297	AC139297 Mus muscu
c1163	19	0.8	206817	2	AC128877	AC128877 Rattus no
c1164	19	0.8	206924	10	AC087780	AC087780 Mus muscu
c1165	19	0.8	207058	5	BX004794	BX004794 Zebrafish
1166	19	0.8	207199	2	CR376853	CR376853 Danio rer
c1167	19	0.8	207743	4	AC121066	AC121066 Oryctolag
c1168	19	0.8	207957	2	AC113746	AC113746 Rattus no
c1169	19	0.8	208229	2	CR388416	CR388416 Danio rer
1170	19	0.8	208296	2	AC099124	AC099124 Rattus no
c1171	19	0.8	208333	2	AC112848	AC112848 Rattus no
1172	19	0.8	208445	2	AC136119	AC136119 Rattus no
c1173	19	0.8	208678	10	AC116575	AC116575 Mus muscu
c1174	19	0.8	208685	2	AC145726	AC145726 Zea mays
1175	19	0.8	208963	2	BX936390	BX936390 Danio rer
1176	19	0.8	209083	10	AC113999	AC113999 Mus muscu
c1177	19	0.8	209112	9	AC010252	AC010252 Homo sapi
1178	19	0.8	209153	2	BX324130	BX324130 Danio rer
1179	19	0.8	209157	2	AC110856	AC110856 Rattus no
c1180	19	0.8	209258	2	AC151027	AC151027 Callithri
1181	19	0.8	209416	2	AC149219	AC149219 Mus muscu
c1182	19	0.8	209866	2	BX546466	BX546466 Danio rer
1183	19	0.8	209927	2	AC150904	AC150904 Pan trogl
c1184	19	0.8	210201	2	CR847962	CR847962 Danio rer
c1185	19	0.8	210320	9	AC093873	AC093873 Homo sapi
1186	19	0.8	210532	9	AC008558	AC008558 Homo sapi
c1187	19	0.8	210793	2	AC109120	AC109120 Rattus no
1188	19	0.8	211251	2	AC121029	AC121029 Rattus no
c1189	19	0.8	211349	10	AL627102	AL627102 Mouse DNA
c1190	19	0.8	211657	10	AL732564	AL732564 Mouse DNA
1191	19	0.8	211910	10	AC116573	AC116573 Mus muscu
c1192	19	0.8	211926	10	AC111092	AC111092 Mus muscu
c1193	19	0.8	212314	5	BX248090	BX248090 Zebrafish
1194	19	0.8	213015	2	AC118195	AC118195 Mus muscu
1195	19	0.8	213439	2	AC149849	AC149849 Papio anu
c1196	19	0.8	213684	10	AC132616	AC132616 Mus muscu
1197	19	0.8	214061	10	AL732571	AL732571 Mouse DNA
c1198	19	0.8	214071	10	AC113102	AC113102 Mus muscu
c1199	19	0.8	214399	10	AC147156	AC147156 Mus muscu
1200	19	0.8	214610	2	BX323578	BX323578 Danio rer

c1201	19	0.8	214610	2	BX323578	BX323578 Danio rer
c1202	19	0.8	215251	10	AC124183	AC124183 Mus muscu
1203	19	0.8	215499	2	BX511257	BX511257 Danio rer
1204	19	0.8	216069	2	AC122086	AC122086 Rattus no
c1205	19	0.8	216878	10	AC147109	AC147109 Mus muscu
c1206	19	0.8	216958	2	AC126465	AC126465 Rattus no
c1207	19	0.8	217278	10	AL604024	AL604024 Mouse DNA
c1208	19	0.8	217384	2	AC023573	AC023573 Homo sapi
1209	19	0.8	217829	10	AL840637	AL840637 Mouse DNA
c1210	19	0.8	218157	2	AC134263	AC134263 Rattus no
c1211	19	0.8	218226	2	AC126634	AC126634 Rattus no
1212	19	0.8	218427	10	AL645727	AL645727 Mouse DNA
1213	19	0.8	218442	2	AC135652	AC135652 Rattus no
1214	19	0.8	218988	2	AC129861	AC129861 Rattus no
c1215	19	0.8	219129	2	AC142415	AC142415 Mus muscu
1216	19	0.8	219341	2	AC114172	AC114172 Rattus no
c1217	19	0.8	219344	2	AC087864	AC087864 Homo sapi
c1218	19	0.8	219616	2	AC112398	AC112398 Rattus no
1219	19	0.8	220612	2	AC112466	AC112466 Rattus no
1220	19	0.8	220788	2	AC130904	AC130904 Rattus no
c1221	19	0.8	221004	9	CNS01DRW	AL121576 Human chr
1222	19	0.8	221128	10	AC123846	AC123846 Mus muscu
c1223	19	0.8	221356	2	AC130588	AC130588 Rattus no
c1224	19	0.8	221801	2	AC128780	AC128780 Rattus no
c1225	19	0.8	221972	2	CR388218	CR388218 Danio rer
c1226	19	0.8	222571	2	AC110338	AC110338 Rattus no
c1227	19	0.8	222814	10	AC134591	AC134591 Mus muscu
1228	19	0.8	223295	2	BX649623	BX649623 Homo sapi
1229	19	0.8	223513	2	AC111919	AC111919 Rattus no
c1230	19	0.8	223630	2	AC130986	AC130986 Rattus no
1231	19	0.8	223730	2	AC140553	AC140553 Mus muscu
c1232	19	0.8	223744	2	CR450774	CR450774 Danio rer
c1233	19	0.8	223890	2	AC062008	AC062008 Homo sapi
1234	19	0.8	223979	2	AC096151	AC096151 Rattus no
1235	19	0.8	224100	2	AC119827	AC119827 Mus muscu
c1236	19	0.8	224451	2	AC132772	AC132772 Rattus no
c1237	19	0.8	224514	2	CR376802	CR376802 Danio rer
c1238	19	0.8	224552	2	AC134092	AC134092 Rattus no
c1239	19	0.8	225035	10	AC145598	AC145598 Mus muscu
c1240	19	0.8	225089	2	AC126666	AC126666 Rattus no
1241	19	0.8	225187	2	AC094836	AC094836 Rattus no
1242	19	0.8	225300	2	AC084798	AC084798 Mus muscu
c1243	19	0.8	225846	2	AC109040	AC109040 Rattus no
1244	19	0.8	225865	2	AC118678	AC118678 Mus muscu
c1245	19	0.8	225893	2	AC103259	AC103259 Rattus no
c1246	19	0.8	226027	2	AC107580	AC107580 Rattus no
c1247	19	0.8	226581	2	AC128234	AC128234 Rattus no
c1248	19	0.8	226589	2	AC117299	AC117299 Rattus no
1249	19	0.8	226631	2	AC025501	AC025501 Mus muscu
c1250	19	0.8	226696	9	AC139026	AC139026 Homo sapi
1251	19	0.8	226740	2	AC112661	AC112661 Mus muscu
c1252	19	0.8	226740	2	AC112661	AC112661 Mus muscu
1253	19	0.8	226891	2	AC120396	AC120396 Mus muscu
c1254	19	0.8	226891	2	AC120396	AC120396 Mus muscu
c1255	19	0.8	227401	2	AC106650	AC106650 Rattus no
c1256	19	0.8	227454	10	AC027700	AC027700 Mus muscu
c1257	19	0.8	227616	2	AC103525	AC103525 Rattus no

1258	19	0.8	227665	2	AC133323	AC133323 Rattus no
1259	19	0.8	227696	2	AC112936	AC112936 Mus muscu
c1260	19	0.8	228182	2	AC109615	AC109615 Mus muscu
c1261	19	0.8	228436	2	AC108544	AC108544 Rattus no
1262	19	0.8	228444	10	AL844147	AL844147 Mouse DNA
c1263	19	0.8	228508	5	AB102768	AB102768 Oryzias l
c1264	19	0.8	228752	2	AC094632	AC094632 Rattus no
1265	19	0.8	228947	2	AC111430	AC111430 Rattus no
1266	19	0.8	229212	2	AC114168	AC114168 Rattus no
c1267	19	0.8	229315	2	AC105651	AC105651 Rattus no
c1268	19	0.8	229548	2	AC106974	AC106974 Rattus no
c1269	19	0.8	229612	2	AL161647	AL161647 Homo sapi
1270	19	0.8	229661	2	AC124474	AC124474 Mus muscu
1271	19	0.8	229792	2	AC113825	AC113825 Rattus no
c1272	19	0.8	230067	2	AC095377	AC095377 Rattus no
1273	19	0.8	230417	2	AC120447	AC120447 Rattus no
1274	19	0.8	230659	2	AC150012	AC150012 Callithri
1275	19	0.8	231234	2	AC134014	AC134014 Rattus no
c1276	19	0.8	231303	5	BX649405	BX649405 Zebrafish
c1277	19	0.8	232184	2	AC103006	AC103006 Rattus no
c1278	19	0.8	232369	2	AC122598	AC122598 Rattus no
1279	19	0.8	233157	2	AC105468	AC105468 Rattus no
1280	19	0.8	233399	2	AC129412	AC129412 Rattus no
c1281	19	0.8	233924	10	AC134579	AC134579 Mus muscu
1282	19	0.8	233992	2	AC094047	AC094047 Rattus no
c1283	19	0.8	233997	2	AC128367	AC128367 Rattus no
c1284	19	0.8	233997	10	AL606521	AL606521 Mouse DNA
c1285	19	0.8	234009	2	CR383672	CR383672 Danio rer
1286	19	0.8	234047	2	AC096460	AC096460 Rattus no
c1287	19	0.8	234160	2	AC117890	AC117890 Rattus no
1288	19	0.8	234344	2	BX323797	BX323797 Danio rer
c1289	19	0.8	234518	2	AC107719	AC107719 Mus muscu
1290	19	0.8	234698	2	AC114581	AC114581 Mus muscu
1291	19	0.8	234939	2	AC094809	AC094809 Rattus no
c1292	19	0.8	235259	2	AC118945	AC118945 Rattus no
c1293	19	0.8	235547	2	AC112586	AC112586 Rattus no
1294	19	0.8	235638	2	AC097984	AC097984 Rattus no
1295	19	0.8	235652	2	AC123474	AC123474 Rattus no
c1296	19	0.8	236275	2	AC120624	AC120624 Rattus no
1297	19	0.8	236385	2	AC094936	AC094936 Rattus no
c1298	19	0.8	237082	10	AL671229	AL671229 Mouse DNA
c1299	19	0.8	237293	2	AC120666	AC120666 Rattus no
1300	19	0.8	237329	2	AC151386	AC151386 Callithri
c1301	19	0.8	237344	2	AC096256	AC096256 Rattus no
1302	19	0.8	237422	5	BX546500	BX546500 Zebrafish
1303	19	0.8	237569	5	BX649547	BX649547 Zebrafish
c1304	19	0.8	237581	2	AC131646	AC131646 Rattus no
c1305	19	0.8	237876	10	AC124601	AC124601 Mus muscu
1306	19	0.8	238046	2	AC109052	AC109052 Rattus no
c1307	19	0.8	238116	2	AC114050	AC114050 Rattus no
c1308	19	0.8	238478	2	AC133432	AC133432 Rattus no
c1309	19	0.8	238850	2	AC094265	AC094265 Rattus no
c1310	19	0.8	238877	2	AC115347	AC115347 Rattus no
1311	19	0.8	238973	2	AC133265	AC133265 Rattus no
1312	19	0.8	239029	2	AC127670	AC127670 Rattus no
1313	19	0.8	239054	2	AC139513	AC139513 Mus muscu
c1314	19	0.8	239113	2	AC094034	AC094034 Rattus no

c1315	19	0.8	239190	2	AC098990	AC098990 Rattus no
1316	19	0.8	239339	2	AC091703	AC091703 Mus muscu
1317	19	0.8	239946	2	AC103505	AC103505 Rattus no
c1318	19	0.8	240004	2	AC113960	AC113960 Mus muscu
1319	19	0.8	240093	2	AC112358	AC112358 Rattus no
1320	19	0.8	240272	2	AC097809	AC097809 Rattus no
c1321	19	0.8	241137	2	AC112078	AC112078 Rattus no
c1322	19	0.8	241199	2	AC105526	AC105526 Rattus no
1323	19	0.8	241418	2	AC098054	AC098054 Rattus no
1324	19	0.8	241616	10	AC129191	AC129191 Mus muscu
1325	19	0.8	241753	2	AC019149	AC019149 Homo sapi
1326	19	0.8	242347	10	AC107789	AC107789 Mus muscu
c1327	19	0.8	242739	2	AC106316	AC106316 Rattus no
1328	19	0.8	242820	2	AC093939	AC093939 Rattus no
1329	19	0.8	242832	10	AC117584	AC117584 Mus muscu
1330	19	0.8	243073	2	AC108537	AC108537 Rattus no
c1331	19	0.8	243124	2	AC097249	AC097249 Rattus no
1332	19	0.8	243422	2	AC098453	AC098453 Rattus no
1333	19	0.8	243556	2	AC114066	AC114066 Rattus no
1334	19	0.8	243804	2	AC136662	AC136662 Rattus no
1335	19	0.8	244050	2	AY657028	AY657028 Mus muscu
1336	19	0.8	244130	2	AC125658	AC125658 Rattus no
1337	19	0.8	244268	2	AC129795	AC129795 Rattus no
c1338	19	0.8	244278	2	AC094685	AC094685 Rattus no
1339	19	0.8	244573	2	AC133400	AC133400 Rattus no
1340	19	0.8	244675	2	AC094935	AC094935 Rattus no
1341	19	0.8	244693	2	AC132971	AC132971 Rattus no
1342	19	0.8	244721	2	AC107195	AC107195 Rattus no
c1343	19	0.8	245283	2	AC096351	AC096351 Rattus no
1344	19	0.8	246384	2	AC108543	AC108543 Rattus no
1345	19	0.8	246630	2	AC095178	AC095178 Rattus no
c1346	19	0.8	246886	2	AC108560	AC108560 Rattus no
c1347	19	0.8	247187	2	AC094928	AC094928 Rattus no
c1348	19	0.8	247208	2	AC120766	AC120766 Rattus no
1349	19	0.8	247451	2	AC097417	AC097417 Rattus no
1350	19	0.8	247936	2	AC112533	AC112533 Rattus no
1351	19	0.8	247961	10	AC016814	AC016814 Mus muscu
c1352	19	0.8	248329	2	AC109989	AC109989 Rattus no
1353	19	0.8	248379	2	AC110341	AC110341 Rattus no
1354	19	0.8	250169	2	AC126583	AC126583 Rattus no
1355	19	0.8	250353	10	AL590969	AL590969 Mouse DNA
1356	19	0.8	250586	2	AC126536	AC126536 Rattus no
1357	19	0.8	250999	2	AC119009	AC119009 Rattus no
1358	19	0.8	251050	5	BX323060	BX323060 Zebrafish
c1359	19	0.8	252148	2	AC127936	AC127936 Rattus no
c1360	19	0.8	253142	2	AC128641	AC128641 Rattus no
c1361	19	0.8	253148	2	AC098015	AC098015 Rattus no
1362	19	0.8	253297	2	AC134076	AC134076 Rattus no
1363	19	0.8	253474	2	AC095441	AC095441 Rattus no
c1364	19	0.8	253712	2	AC095520	AC095520 Rattus no
c1365	19	0.8	255924	2	AC096518	AC096518 Rattus no
1366	19	0.8	257396	2	AC130569	AC130569 Rattus no
c1367	19	0.8	257595	2	AC123011	AC123011 Rattus no
c1368	19	0.8	258847	2	AC112746	AC112746 Rattus no
1369	19	0.8	259123	2	AC108237	AC108237 Rattus no
1370	19	0.8	259720	2	AC094497	AC094497 Rattus no
1371	19	0.8	259762	2	AC102615	AC102615 Mus muscu

c1372	19	0.8	259970	2	AC106985	AC106985 Rattus no
1373	19	0.8	260241	2	AC105158	AC105158 Mus muscu
c1374	19	0.8	261498	2	AC073823	AC073823 Mus muscu
c1375	19	0.8	262032	2	AC131396	AC131396 Rattus no
1376	19	0.8	262050	2	AC105575	AC105575 Rattus no
1377	19	0.8	262124	2	AC095111	AC095111 Rattus no
1378	19	0.8	262142	2	AC095654	AC095654 Rattus no
c1379	19	0.8	263730	2	AC094314	AC094314 Rattus no
1380	19	0.8	263954	2	AC117122	AC117122 Rattus no
1381	19	0.8	264380	2	AC120824	AC120824 Rattus no
c1382	19	0.8	266926	2	AC112028	AC112028 Rattus no
1383	19	0.8	266973	2	AC109414	AC109414 Rattus no
c1384	19	0.8	267328	2	AC110688	AC110688 Rattus no
1385	19	0.8	267749	2	AC131472	AC131472 Rattus no
1386	19	0.8	267795	2	AC096390	AC096390 Rattus no
1387	19	0.8	268663	2	AC110147	AC110147 Rattus no
c1388	19	0.8	269229	2	AC097551	AC097551 Rattus no
1389	19	0.8	269301	2	AC102913	AC102913 Mus muscu
1390	19	0.8	270086	2	AC128132	AC128132 Rattus no
1391	19	0.8	270108	2	AC125642	AC125642 Rattus no
1392	19	0.8	271429	2	AC129086	AC129086 Rattus no
c1393	19	0.8	272336	2	AC128072	AC128072 Rattus no
1394	19	0.8	272698	3	PFMAL4P4	AL035477 Plasmodiu
1395	19	0.8	273413	2	AC079314	AC079314 Homo sapi
c1396	19	0.8	273715	2	AC140797	AC140797 Mus muscu
1397	19	0.8	273722	2	AC098260	AC098260 Rattus no
c1398	19	0.8	275111	2	AC115133	AC115133 Rattus no
1399	19	0.8	275900	2	AC103476	AC103476 Rattus no
1400	19	0.8	276787	2	AC113850	AC113850 Rattus no
c1401	19	0.8	277124	2	AC132639	AC132639 Rattus no
c1402	19	0.8	277196	9	AE014302	AE014302 Homo sapi
1403	19	0.8	277220	2	AC097838	AC097838 Rattus no
c1404	19	0.8	278206	2	AL513471	AL513471 Homo sapi
c1405	19	0.8	279232	2	AC120754	AC120754 Rattus no
c1406	19	0.8	282610	2	AC096244	AC096244 Rattus no
c1407	19	0.8	282788	2	AC120748	AC120748 Rattus no
c1408	19	0.8	286007	2	BX942834	BX942834 Danio rer
1409	19	0.8	286448	2	AC116760	AC116760 Mus muscu
1410	19	0.8	288728	2	AC099368	AC099368 Rattus no
c1411	19	0.8	289545	2	AC096832	AC096832 Rattus no
1412	19	0.8	289893	3	AE003576	AE003576 Drosophil
c1413	19	0.8	290029	1	AE017134	AE017134 Yersinia
1414	19	0.8	290128	2	AC124325	AC124325 Mus muscu
1415	19	0.8	296756	3	AE003492	AE003492 Drosophil
c1416	19	0.8	296756	3	AE003492	AE003492 Drosophil
c1417	19	0.8	297235	2	AL499603	AL499603 Homo sapi
c1418	19	0.8	297984	2	AC099152	AC099152 Rattus no
c1419	19	0.8	300000	9	AP002530	AP002530 Homo sapi
1420	19	0.8	300201	2	AC107086	AC107086 Rattus no
1421	19	0.8	300988	2	AC096249	AC096249 Rattus no
c1422	19	0.8	301450	1	AP003185	AP003185 Clostridi
1423	19	0.8	304230	1	AE016940	AE016940 Bacteroid
1424	19	0.8	305900	3	AE003590	AE003590 Drosophil
c1425	19	0.8	309662	2	AC004469	AC004469 Homo sapi
1426	19	0.8	313378	2	AC094200	AC094200 Rattus no
1427	19	0.8	318503	2	AC074166	AC074166 Mus muscu
c1428	19	0.8	319367	10	AC021709	AC021709 Mus muscu

1429	19	0.8	321250	1	MPULM02	AL445564 Mycoplasm
1430	19	0.8	322101	6	AX814520	AX814520 Sequence
c1431	19	0.8	329753	2	AC096701	AC096701 Rattus no
c1432	19	0.8	331448	2	AC134126	AC134126 Rattus no
c1433	19	0.8	334050	1	AJ414151	AJ414151 Yersinia
c1434	19	0.8	336609	1	BX571867	BX571867 Photorhab
1435	19	0.8	336873	2	AC104875	AC104875 Mus muscu
1436	19	0.8	338197	2	AC151283	AC151283 Mus muscu
c1437	19	0.8	340000	9	HS21C084	AL163284 Homo sapi
1438	19	0.8	346357	1	BX842647	BX842647 Bdellovib
c1439	19	0.8	346542	2	AC120727	AC120727 Rattus no
c1440	19	0.8	347572	2	AC107303	AC107303 Homo sapi
1441	19	0.8	349080	1	CR378667	CR378667 Photobact
c1442	19	0.8	349980	6	CQ870214	CQ870214 Sequence
1443	19	0.8	349980	6	CQ870217	CQ870217 Sequence
1444	19	0.8	349980	6	AX571765	AX571765 Sequence
1445	19	0.8	349980	6	AX770905	AX770905 Sequence
1446	18	0.8	18	6	AX697385	AX697385 Sequence
1447	18	0.8	90	6	CQ809145	CQ809145 Sequence
c1448	18	0.8	100	6	AX989875	AX989875 Sequence
c1449	18	0.8	100	6	AX989876	AX989876 Sequence
1450	18	0.8	128	11	G31764	G31764 sWSS3153 Er
1451	18	0.8	189	6	CQ740741	CQ740741 Sequence
1452	18	0.8	189	11	BV101285	BV101285 RPAMMSEQ0
1453	18	0.8	201	11	BV201536	BV201536 sqnm20683
1454	18	0.8	201	11	BV208102	BV208102 sqnm22547
1455	18	0.8	201	11	BV208103	BV208103 sqnm22547
1456	18	0.8	211	3	TRFKPB	M18394 C.fascicula
c1457	18	0.8	227	9	HUMMSP03	M34375 Homo sapien
c1458	18	0.8	250	3	MICFMNC3	X04483 Critidia fa
1459	18	0.8	269	3	CFKTAA	X66923 C.fascicula
c1460	18	0.8	302	9	AF535053	AF535053 Otolemur
c1461	18	0.8	303	6	AR083938	AR083938 Sequence
c1462	18	0.8	303	9	AF113846	AF113846 Homo sapi
c1463	18	0.8	323	5	AY330910	AY330910 Scaphiopu
1464	18	0.8	333	6	CQ731579	CQ731579 Sequence
c1465	18	0.8	337	5	AF402880	AF402880 Acipenser
c1466	18	0.8	337	5	AF402881	AF402881 Acipenser
c1467	18	0.8	337	5	AF402882	AF402882 Acipenser
c1468	18	0.8	337	5	AF402883	AF402883 Acipenser
c1469	18	0.8	337	5	AF402884	AF402884 Acipenser
c1470	18	0.8	337	5	AF402885	AF402885 Acipenser
c1471	18	0.8	337	5	AF402886	AF402886 Acipenser
c1472	18	0.8	337	5	AF402887	AF402887 Acipenser
c1473	18	0.8	337	5	AF402888	AF402888 Acipenser
c1474	18	0.8	337	5	AF402889	AF402889 Acipenser
c1475	18	0.8	337	5	AF402890	AF402890 Acipenser
c1476	18	0.8	337	5	AF402891	AF402891 Acipenser
c1477	18	0.8	337	5	AF402892	AF402892 Acipenser
c1478	18	0.8	337	5	AF402893	AF402893 Acipenser
c1479	18	0.8	337	5	AF402894	AF402894 Acipenser
c1480	18	0.8	337	5	AF402895	AF402895 Acipenser
c1481	18	0.8	337	5	AF402896	AF402896 Huso daur
c1482	18	0.8	337	5	AF402897	AF402897 Huso huso
c1483	18	0.8	337	5	AF402898	AF402898 Pseudosca
c1484	18	0.8	337	5	AF402899	AF402899 Pseudosca
c1485	18	0.8	337	5	AF402900	AF402900 Scaphirhy

c1486	18	0.8	337	5	AF402901	AF402901 Scaphirhy
c1487	18	0.8	337	5	AF402902	AF402902 Scaphirhy
c1488	18	0.8	337	5	AF402903	AF402903 Polyodon
c1489	18	0.8	337	5	AF402904	AF402904 Psephurus
c1490	18	0.8	346	5	MTSH12S1	X86226 S.holbrooki
c1491	18	0.8	355	5	AY430247	AY430247 Scaphirhy
1492	18	0.8	358	4	AF511171	AF511171 Sus scrof
c1493	18	0.8	358	11	BV060954	BV060954 S212P6013
1494	18	0.8	361	6	BD059704	BD059704 Secreted
1495	18	0.8	376	11	G64820	G64820 B102I13.GSS
1496	18	0.8	386	11	AB165494	AB165494 Bos tauru
c1497	18	0.8	387	5	ANY12664	Y12664 Acipenser n
c1498	18	0.8	391	5	ABU86710	U86710 Acipenser b
c1499	18	0.8	399	6	CQ459477	CQ459477 Sequence
1500	18	0.8	402	6	AX224134	AX224134 Sequence

ALIGNMENTS

RESULT 1
AX697213
LOCUS AX697213 2320 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 281 from Patent WO0078961.
ACCESSION AX697213
VERSION AX697213.1 GI:29498151
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0078961-A 281 28-DEC-2000;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1. .2320
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 2320; DB 6; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy         61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

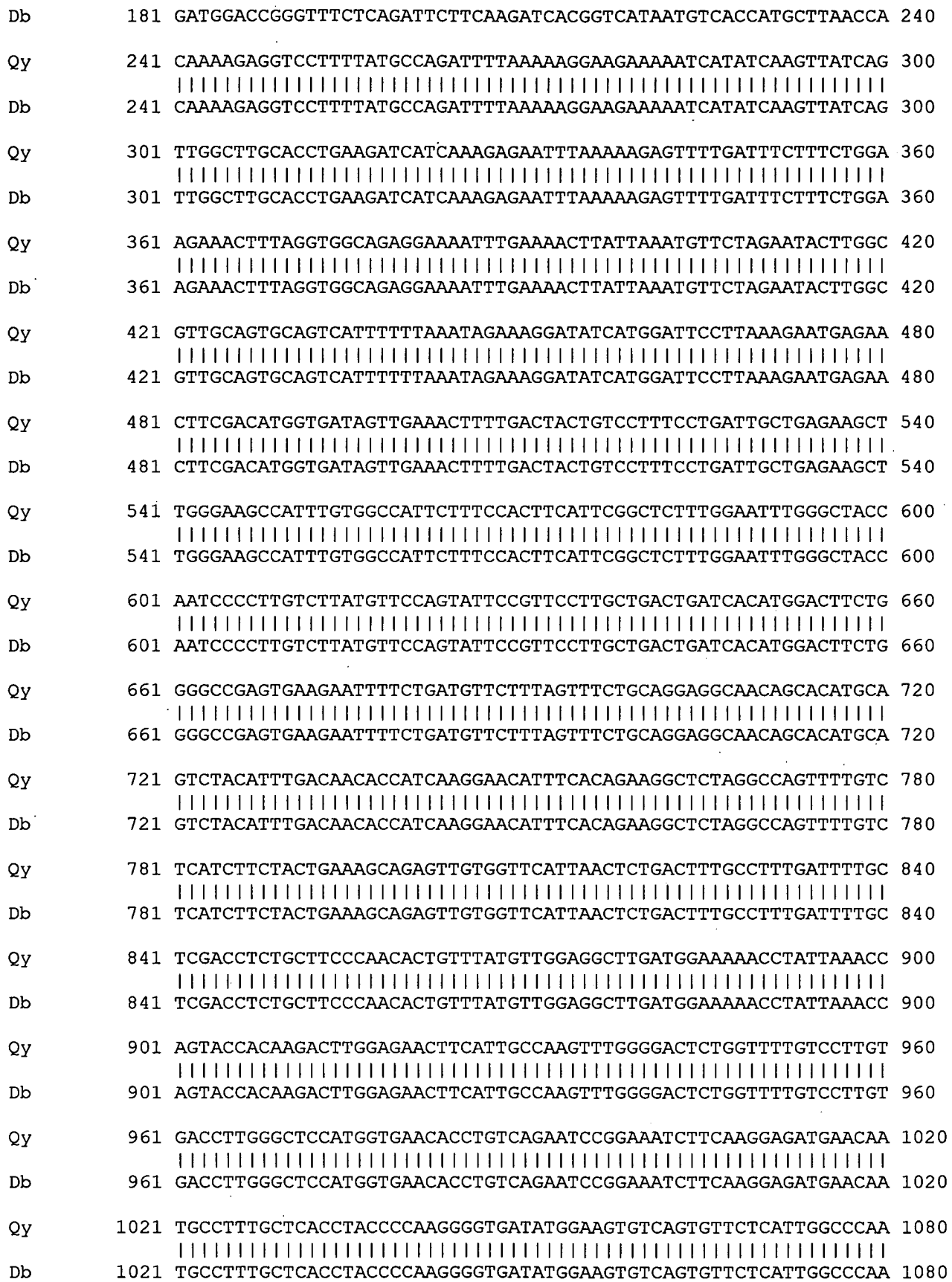
```
Db        61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy       121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy       181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

Qy       241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300

Qy       301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360

Qy       361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 420

Qy       421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480

Qy       481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

Qy       541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600

Qy       601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 660

Qy       661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720

Qy       721 GTCTACATTTGACAACACCATCAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GTCTACATTTGACAACACCATCAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTC 780

Qy       781 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC 840

Qy       841 TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC 900

Qy       901 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT 960
```

```
Qy        961 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA 1020

Qy       1021 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA 1080

Qy       1081 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1140

Qy       1141 GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC 1200

Qy       1201 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1260

Qy       1261 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1320

Qy       1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380

Qy       1381 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440

Qy       1441 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500

Qy       1501 GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560

Qy       1561 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1620

Qy       1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680

Qy       1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740

Qy       1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1800
```

```
Qy       1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860

Qy       1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920

Qy       1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980

Qy       1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040

Qy       2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100

Qy       2101 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

Qy       2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220

Qy       2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280

Qy       2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
             ||||||||||||||||||||||||||||||||||||||||
Db       2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
```

```
RESULT 2
AY358416
LOCUS       AY358416               2320 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA71169 glucuronosyltransferase (UNQ842) mRNA,
            complete cds.
ACCESSION   AY358416
VERSION     AY358416.1  GI:37181956
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2320)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
```

```
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 2320)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .2320
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DNA71169"
     gene            1. .2320
                     /locus_tag="UNQ842"
     CDS             68. .1639
                     /locus_tag="UNQ842"
                     /note="PRO1780"
                     /codon_start=1
                     /product="glucuronosyltransferase"
                     /protein_id="AAQ88782.1"
                     /db_xref="GI:37181957"
                     /translation="MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQ
                     ILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLG
                     GRGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGK
                     PFVAILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQ
                     STFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLPNTVYVGGLMEKPI
                     KPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCS
                     HWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFG
                     DQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLS
                     PTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDVFVFLLGLTLGTLWLCGKLLG
                     MAVWWLRGARKVKET"
ORIGIN

  Query Match             100.0%;  Score 2320;  DB 9;  Length 2320;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy         61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

Qy        121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

Qy        181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```



```
Qy       1081 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1140

Qy       1141 GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC 1200

Qy       1201 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1260

Qy       1261 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1320

Qy       1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380

Qy       1381 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440

Qy       1441 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500

Qy       1501 GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560

Qy       1561 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1620

Qy       1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680

Qy       1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740

Qy       1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1800

Qy       1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860

Qy       1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
```

```
Qy       1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980

Qy       1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040

Qy       2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100

Qy       2101 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

Qy       2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220

Qy       2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280

Qy       2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
             ||||||||||||||||||||||||||||||||||||||||
Db       2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
```

```
RESULT 3
AX136141
LOCUS       AX136141                2341 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 63 from Patent EP1067182.
ACCESSION   AX136141
VERSION     AX136141.1  GI:14272549
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
            Hayashi,K.
  TITLE     Secretory protein or membrane protein
  JOURNAL   Patent: EP 1067182-A 63 10-JAN-2001;
            Helix Research Institute (JP)
FEATURES             Location/Qualifiers
     source          1. .2341
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             94. .1665
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC39713.1"
                     /db_xref="GI:14272550"
                     /translation="MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQ
```

ILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLG
GRGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGK
PFVAILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQ
STFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLPNTVYVGGLMEKPI
KPVPQDLENFIAKFEDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCS
HWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFG
DQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLS
PTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLLDVFVFLLGLTLGTLWLCGKLLG
MAVWWLRGARKVKET"

ORIGIN

Query Match 93.2%; Score 2162; DB 6; Length 2341;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 86

Qy         61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 146

Qy        121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 206

Qy        181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 266

Qy        241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 326

Qy        301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 386

Qy        361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 446

Qy        421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 506

Qy        481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 566

Qy        541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 626

Qy        601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        627 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 686

Qy        661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 746

Qy        721 GTCTACATTTGACAACACCATCAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GTCTACATTTGACAACACCATCAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTC 806

Qy        781 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC 866

Qy        841 TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC 926

Qy        901 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT 960
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        927 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGAGGACTCTGGTTTTGTCCTTGT 986

Qy        961 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA 1046

Qy       1021 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1047 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA 1106

Qy       1081 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1107 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1166

Qy       1141 GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1167 GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC 1226

Qy       1201 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1227 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1286

Qy       1261 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1287 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1346

Qy       1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1347 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1406

Qy       1381 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1407 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1466

Qy       1441 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1467 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1526
```

```
Qy       1501 GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1527 GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1586

Qy       1561 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1587 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1646

Qy       1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1647 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1706

Qy       1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1707 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1766

Qy       1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1767 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1826

Qy       1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1827 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAATTCTTTCCAGTCCT 1886

Qy       1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1887 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1946

Qy       1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1947 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 2006

Qy       1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2007 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2066

Qy       2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2067 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2126

Qy       2101 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2127 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2186

Qy       2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2187 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2246

Qy       2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2247 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2306

Qy       2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2315
             |||||||||||||||||||||||||||||||||
Db       2307 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2341
```

RESULT 4
BD123523
LOCUS BD123523 2341 bp DNA linear PAT 18-SEP-2002
DEFINITION Secretory protein or membrane protein.
ACCESSION BD123523
VERSION BD123523.1 GI:23218468
KEYWORDS JP 2002017376-A/32.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2341)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: JP 2002017376-A 32 22-JAN-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017376-A/32
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253173
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
PI SUGIYAMA,
PI KOJI HAYASHI
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC
Secretory protein or membrane protein
FH Key Location/Qualifiers
FT CDS (94). .(1662).
FEATURES Location/Qualifiers
source 1. .2341
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 93.2%; Score 2162; DB 6; Length 2341;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 86

Qy         61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 146

Qy        121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 206

Qy        181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        207 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 266

Qy        241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 326

Qy        301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 386

Qy        361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGC 446

Qy        421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA 506

Qy        481 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 566

Qy        541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 626

Qy        601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTG 686

Qy        661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 746

Qy        721 GTCTACATTTGACAACACCATCAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GTCTACATTTGACAACACCATCAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTC 806

Qy        781 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGC 866

Qy        841 TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC 926

Qy        901 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT 960
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        927 AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGAGGACTCTGGTTTTGTCCTTGT 986

Qy        961 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA 1046

Qy       1021 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1047 TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA 1106
```

```
Qy       1081 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1107 AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT 1166

Qy       1141 GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1167 GGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGC 1226

Qy       1201 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1227 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1286

Qy       1261 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1287 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1346

Qy       1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1347 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1406

Qy       1381 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1407 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1466

Qy       1441 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1467 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1526

Qy       1501 GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1527 GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1586

Qy       1561 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1587 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1646

Qy       1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1647 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1706

Qy       1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1707 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1766

Qy       1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1767 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1826

Qy       1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1827 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAATTCTTTCCAGTCCT 1886

Qy       1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1887 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1946
```

```
Qy       1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1947 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 2006

Qy       1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2007 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2066

Qy       2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2067 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2126

Qy       2101 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2127 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2186

Qy       2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2187 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2246

Qy       2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2247 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2306

Qy       2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2315
             |||||||||||||||||||||||||||||||||||
Db       2307 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2341
```

RESULT 5
AK075383

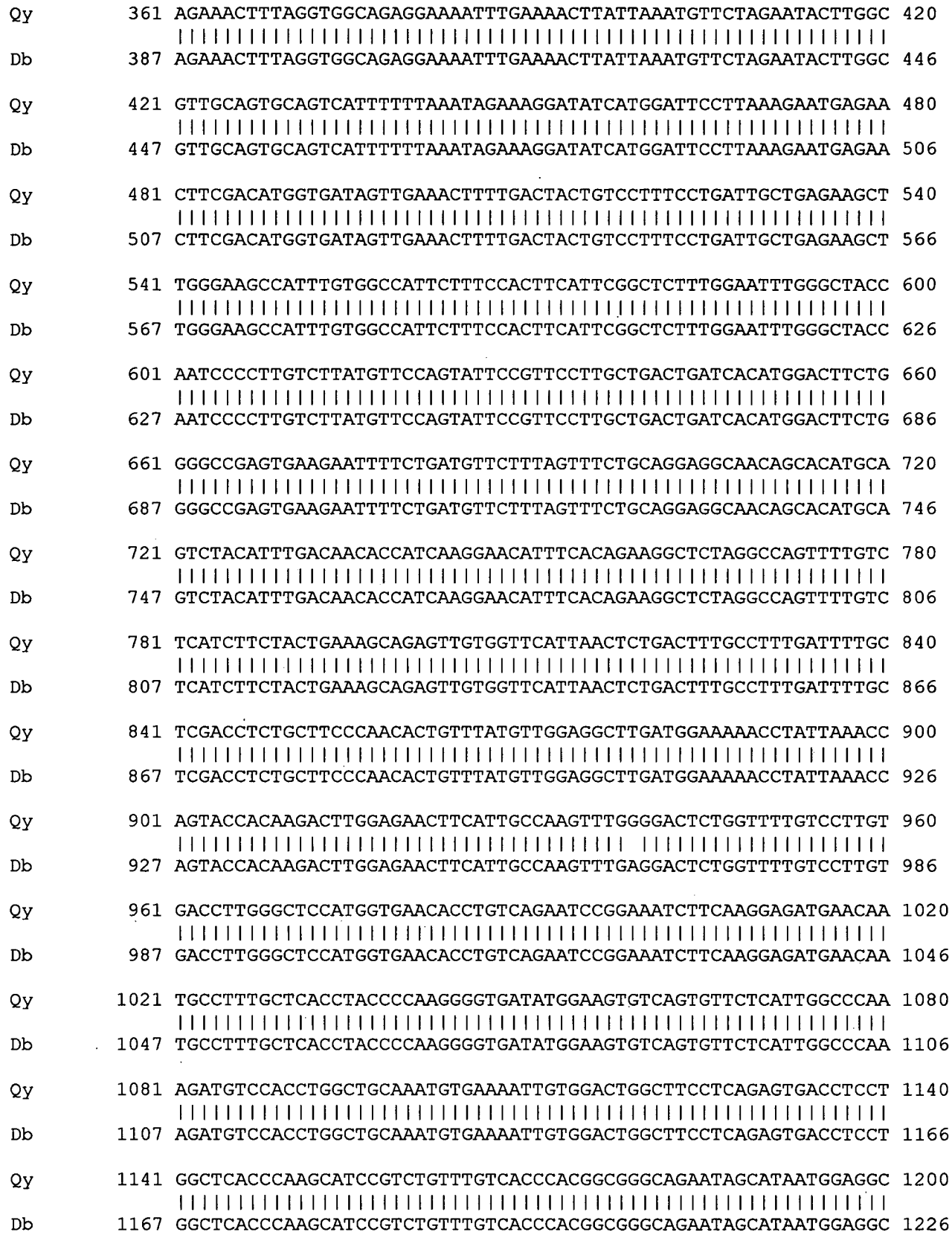
```
LOCUS       AK075383               2341 bp    mRNA    linear   PRI 03-SEP-2002
DEFINITION  Homo sapiens cDNA PSEC0073 fis, clone NT2RP2002934, weakly similar
            to UDP-GLUCURONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17).
ACCESSION   AK075383
VERSION     AK075383.1  GI:22761433
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
            Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
            Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.
  TITLE     HRI human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2341)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
            sequencing, clone selection and full insert sequencing: Helix
            Research Institute (supported by Japan Key Technology Center etc.);
            cDNA library construction: Institute of Medical Science, University
```

of Tokyo, Laboratory of Genome Structure, Human Genome Center.

```
FEATURES             Location/Qualifiers
     source          1. .2341
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="NT2RP2002934"
                     /cell_line="NT2"
                     /cell_type="teratocarcinoma"
                     /clone_lib="NT2RP2"
                     /note="cloning vector: pME18SFL3~mRNA from NT2 neuronal
                     precursor cells after 2-weeks retinoic acid (RA)
                     induction"
     CDS             94. .1665
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="BAC11583.1"
                     /db_xref="GI:22761434"
                     /translation="MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQ
                     ILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLG
                     GRGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGK
                     PFVAILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQ
                     STFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLPNTVYVGGLMEKPI
                     KPVPQDLENFIAKFEDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCS
                     HWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFG
                     DQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLS
                     PTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLLDVFVFLLGLTLGTLWLCGKLLG
                     MAVWWLRGARKVKET"
ORIGIN
```

Query Match 93.2%; Score 2162; DB 9; Length 2341;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 86

Qy         61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 146

Qy        121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 206

Qy        181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 266

Qy        241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 326

Qy        301 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 386
```



```
Qy       1201 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1227 CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT 1286

Qy       1261 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1287 GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGA 1346

Qy       1321 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1347 GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT 1406

Qy       1381 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1407 GGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG 1466

Qy       1441 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1467 GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA 1526

Qy       1501 GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1560
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1527 GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG 1586

Qy       1561 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1587 GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG 1646

Qy       1621 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1647 AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG 1706

Qy       1681 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1707 TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT 1766

Qy       1741 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1767 TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA 1826

Qy       1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1827 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAATTCTTTCCAGTCCT 1886

Qy       1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1887 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1946

Qy       1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1947 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 2006

Qy       1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2007 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2066

Qy       2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2067 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2126

Qy       2101 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2127 TTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2186

Qy       2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2187 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2246

Qy       2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2247 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAA 2306

Qy       2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2315
                |||||||||||||||||||||||||||||||||
Db       2307 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2341


RESULT 6
AX548037
LOCUS       AX548037                2944 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 13 from Patent WO02066654.
ACCESSION   AX548037
VERSION     AX548037.1  GI:25813133
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Astromoff,A., Au-Young,J., Baughn,M.R., Ding,L., Duggan,B.M.,
            Forsythe,I.J., Gietzen,K.J., Griffin,J.A., Lee,E.A., Lu,Y.,
            Richardson,T.W., Ring,H.Z., Sanjanwala,M.M., Swarnakar,A.,
            Walia,N.K., Warren,B.A., Xu,Y., Yue,H. and Zebarjadian,Y.
  TITLE     Drug metabolizing enzymes
  JOURNAL   Patent: WO 02066654-A 13 29-AUG-2002;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2944
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 7486594CB1"
ORIGIN

  Query Match             84.4%;  Score 1957;  DB 6;  Length 2944;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2057;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        262 AGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCACCTGAAGATCA 321
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 AGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCACCTGAAGATCA 422

Qy        322 TCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAAACTTTAGGTGGCAGAGG 381
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        423 TCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAAACTTTAGGTGGCAGAGG 482

Qy        382 AAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTT 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 AAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTT 542

Qy        442 AAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGA 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 AAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGA 602

Qy        502 AACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCAT 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCAT 662

Qy        562 TCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 TCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCC 722

Qy        622 AGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCT 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 AGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCT 782

Qy        682 GATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCAT 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCAT 842

Qy        742 CAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGA 902

Qy        802 GTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACAC 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 GTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACAC 962

Qy        862 TGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAA 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 TGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAA 1022

Qy        922 CTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAA 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 CTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAA 1082

Qy        982 CACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCA 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 CACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCA 1142

Qy       1042 AGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 AGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAA 1202

Qy       1102 TGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCT 1161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 TGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCT 1262

Qy       1162 GTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCAT 1221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 GTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCAT 1322
```

```
Qy       1222 GGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAA 1281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 GGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAA 1382

Qy       1282 GTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAA 1341
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1383 GTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAA 1442

Qy       1342 ACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCG 1401
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1443 ACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCG 1502

Qy       1402 CTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGAC 1461
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 CTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGAC 1562

Qy       1462 AGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCT 1521
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1563 AGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCT 1622

Qy       1522 GTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAA 1581
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 GCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAA 1682

Qy       1582 GCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGG 1641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 GCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGG 1742

Qy       1642 CCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTC 1701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1743 CCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTC 1802

Qy       1702 CCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGA 1761
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1803 CCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGA 1862

Qy       1762 ACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCT 1821
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1863 ACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCT 1922

Qy       1822 TACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCA 1881
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1923 TACTAGCTCCTGCCTGCTAGCAGAATTCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCA 1982

Qy       1882 TCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATT 1941
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1983 TCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATT 2042

Qy       1942 TCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTC 2001
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2043 TCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTC 2102

Qy       2002 CAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGG 2061
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2103 CAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGG 2162
```

```
Qy       2062 AATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACAT 2121
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2163 AATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACAT 2222

Qy       2122 ATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGC 2181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2223 ATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGC 2282

Qy       2182 TCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTG 2241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2283 TCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTG 2342

Qy       2242 AGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTAT 2301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2343 AGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTAT 2402

Qy       2302 CTCTCCCCAACCTCACTAA 2320
             ||||||||||||||||||
Db       2403 CTCTCCCCAACCTCACTAA 2421


RESULT 7
CQ726650
LOCUS       CQ726650                1836 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 12584 from Patent WO02068579.
ACCESSION   CQ726650
VERSION     CQ726650.1  GI:42290368
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 12584 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1836
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             39.0%;  Score 905;  DB 6;  Length 1836;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  905;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        458 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT 60

Qy        518 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTC 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTC 120
```

```
Qy        578 GGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTG 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCTTG 180

Qy        638 CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTC 240

Qy        698 TGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTCACA 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTCACA 300

Qy        758 GAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAC 360

Qy        818 TCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGC 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGC 420

Qy        878 TTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTT 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTT 480

Qy        938 GGGGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCG 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGGACTCTGGTTTTGTCCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCG 540

Qy        998 GAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAG 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAG 600

Qy       1058 TGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGAC 1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGAC 660

Qy       1118 TGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGC 1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCCACGGC 720

Qy       1178 GGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTC 1237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTC 780

Qy       1238 TTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATT 1297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATT 840

Qy       1298 CAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGAC 1357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGAC 900

Qy       1358 AAGAG 1362
              |||||
Db        901 AAGAG 905
```

RESULT 8
AC008947/c
LOCUS AC008947 88948 bp DNA linear HTG 05-MAY-2000
DEFINITION Homo sapiens chromosome 5 clone CTD-2330L9, WORKING DRAFT SEQUENCE, 19 unordered pieces.
ACCESSION AC008947
VERSION AC008947.5 GI:7710868
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 88948)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 88948)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On May 5, 2000 this sequence version replaced gi:6997051.
-------Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 754542
Center clone name: CITB-H1_2330L9

Summary Statistics
Consensus quality: 67454 bases at least Q40
Consensus quality: 80777 bases at least Q30
Consensus quality: 83103 bases at least Q20
Estimated insert size: 85000; pulse field gel estimation
Estimated insert size: 87148; sum-of-contigs estimation
Quality coverage: 3.94 in Q20 bases; pulse field gel estimation
Quality coverage: 3.84 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2375: contig of 2375 bp in length
* 2376 2475: gap of unknown length
* 2476 5577: contig of 3102 bp in length
* 5578 5677: gap of unknown length
* 5678 7838: contig of 2161 bp in length
* 7839 7938: gap of unknown length
* 7939 10123: contig of 2185 bp in length
* 10124 10223: gap of unknown length
* 10224 12755: contig of 2532 bp in length

```
              *    12756    12855: gap of unknown length
              *    12856    15242: contig of 2387 bp in length
              *    15243    15342: gap of unknown length
              *    15343    17589: contig of 2247 bp in length
              *    17590    17689: gap of unknown length
              *    17690    20485: contig of 2796 bp in length
              *    20486    20585: gap of unknown length
              *    20586    23628: contig of 3043 bp in length
              *    23629    23728: gap of unknown length
              *    23729    26745: contig of 3017 bp in length
              *    26746    26845: gap of unknown length
              *    26846    30194: contig of 3349 bp in length
              *    30195    30294: gap of unknown length
              *    30295    34563: contig of 4269 bp in length
              *    34564    34663: gap of unknown length
              *    34664    39707: contig of 5044 bp in length
              *    39708    39807: gap of unknown length
              *    39808    47134: contig of 7327 bp in length
              *    47135    47234: gap of unknown length
              *    47235    52767: contig of 5533 bp in length
              *    52768    52867: gap of unknown length
              *    52868    59030: contig of 6163 bp in length
              *    59031    59130: gap of unknown length
              *    59131    65592: contig of 6462 bp in length
              *    65593    65692: gap of unknown length
              *    65693    75313: contig of 9621 bp in length
              *    75314    75413: gap of unknown length
              *    75414    88948: contig of 13535 bp in length.
FEATURES             Location/Qualifiers
     source          1. .88948
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-2330L9"
                     /clone_lib="CalTech human BAC library D"
ORIGIN

  Query Match             34.8%;  Score 807;  DB 2;  Length 88948;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  957;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1361 AGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCC 1420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4580 AGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCC 4521

Qy       1421 ACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTC 1480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4520 ACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTC 4461

Qy       1481 AAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTT 1540
             |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       4460 AAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTT 4401

Qy       1541 CTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTC 1600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4400 CTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTC 4341
```

```
Qy       1601 TGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGG 1660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4340 TGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGG 4281

Qy       1661 GGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCC 1720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4280 GGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCC 4221

Qy       1721 CATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAA 1780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4220 CATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAA 4161

Qy       1781 ATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTA 1840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4160 ATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTA 4101

Qy       1841 GCAGAAATCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGT 1900
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4100 GCAGAATTCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGT 4041

Qy       1901 GATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACC 1960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4040 GATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACC 3981

Qy       1961 TTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACC 2020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3980 TTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACC 3921

Qy       2021 TAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGAC 2080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3920 TAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGAC 3861

Qy       2081 ACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGG 2140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3860 ACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGG 3801

Qy       2141 AAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGG 2200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3800 AAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGG 3741

Qy       2201 GTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTA 2260
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       3740 GTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCTTGGAGACTGTA 3681

Qy       2261 GGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3680 GGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 3621
```

```
RESULT 9
AC016612
LOCUS       AC016612               179513 bp    DNA     linear   PRI 06-SEP-2001
DEFINITION  Homo sapiens chromosome 5 clone CTD-2197M16, complete sequence.
ACCESSION   AC016612
VERSION     AC016612.6  GI:15451670
KEYWORDS    HTG.
```

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 179513)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 179513)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 179513)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-DEC-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 179513)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Sep 6, 2001 this sequence version replaced gi:11908274.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.4% of Sequence;
            Estimated Total Number of Errors is 0.8.
            STS Content:
            SHGC-141485 G63682
            SHGC-104791 G58536.
FEATURES             Location/Qualifiers
     source          1. .179513
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-2197M16"
ORIGIN

  Query Match             34.8%;  Score 807;  DB 9;  Length 179513;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  957;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1361 AGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCC 1420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48084 AGATACAAGTCCGCGGCAGTGGCTGCCAGTGTCATCCTGCGCTCCCACCCGCTCAGCCCC 48143

Qy       1421 ACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTC 1480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48144 ACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTC 48203

Qy       1481 AAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTT 1540
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db      48204 AAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTT 48263
```

```
Qy       1541 CTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTC 1600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48264 CTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTC 48323

Qy       1601 TGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGG 1660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48324 TGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGG 48383

Qy       1661 GGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCC 1720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48384 GGTCTGTTTGGTGGGCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCC 48443

Qy       1721 CATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAA 1780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48444 CATTCTCTAGTCCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAA 48503

Qy       1781 ATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTA 1840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48504 ATCATCCTTTCCACTTGCTAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTA 48563

Qy       1841 GCAGAAATCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGT 1900
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48564 GCAGAATTCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGT 48623

Qy       1901 GATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACC 1960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48624 GATTCTGTCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACC 48683

Qy       1961 TTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACC 2020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48684 TTCCTTCTCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACC 48743

Qy       2021 TAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGAC 2080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48744 TAGTCAGCCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGAC 48803

Qy       2081 ACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGG 2140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48804 ACCTTGCATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGG 48863

Qy       2141 AAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGG 2200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48864 AAGCCTGCCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGG 48923

Qy       2201 GTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTA 2260
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      48924 GTCCCTGTCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCTTGGAGACTGTA 48983

Qy       2261 GGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48984 GGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 49043
```

RESULT 10
AX958403
LOCUS AX958403 2263 bp DNA linear PAT 14-JAN-2004

```
DEFINITION  Sequence 31 from Patent WO0226988.
ACCESSION   AX958403
VERSION     AX958403.1  GI:40879361
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   .
  TITLE     Human drug metabolizing enzymes
  JOURNAL   Patent: WO 0226988-A 31 04-APR-2002;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2263
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             33.4%;  Score 776;  DB 6;  Length 2263;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  826;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        968 GGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTT 1027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 GGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTT 1042

Qy       1028 GCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAAAGATGTC 1087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 GCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAAAGATGTC 1102

Qy       1088 CACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC 1147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 CACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC 1162

Qy       1148 CCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAG 1207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1163 CCAAGCATCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAG 1222

Qy       1208 CATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGA 1267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1223 CATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGA 1282

Qy       1268 GTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTG 1327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1283 GTAGAAGCCAAAAAGTTTGGTGTTTCTATTCAGTTAAAGAAGCTCAAGGCAGAGACATTG 1342

Qy       1328 GCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCC 1387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1343 GCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCC 1402

Qy       1388 AGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGAC 1447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1403 AGTGTCATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGAC 1462

Qy       1448 CACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGG 1507
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1463 CACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGG 1522

Qy       1508 CATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTA 1567
                ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1523 CATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTA 1582

Qy       1568 TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG 1627
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1583 TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG 1642

Qy       1628 AAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCAT 1687
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1643 AAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATGTCACCAT 1702

Qy       1688 TTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCC 1747
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1703 TTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGTTATCTCC 1762

Qy       1748 TGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCAC 1794
                ||||||||||||||||||||||||||||||||||||||||||||||
Db       1763 TGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCAC 1809
```

```
RESULT 11
AC025476/c
LOCUS       AC025476               148069 bp    DNA     linear   HTG 31-AUG-2001
DEFINITION  Homo sapiens chromosome 5 clone RP11-36A10, WORKING DRAFT SEQUENCE,
            4 unordered pieces.
ACCESSION   AC025476
VERSION     AC025476.5  GI:15290368
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 148069)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Human Chromosome 5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 148069)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAR-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     On Aug 25, 2001 this sequence version replaced gi:13699663.
            -------Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -------
            Project Information
            Center Project Name: 420199
            Center clone name: RPCI-11_36A10
            -------
            Summary Statistics
            Consensus quality: 145481 bases at least Q40
```

```
            Consensus quality: 147102 bases at least Q30
            Consensus quality: 147415 bases at least Q20
            Estimated insert size: 147360; agarose-fp estimation
            Estimated insert size: 147769; sum-of-contigs estimation
            Quality coverage:  5.89 in Q20 bases; agarose-fp estimation
            Quality coverage:  5.88 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     8195: contig of 8195 bp in length
            *     8196     8295: gap of unknown length
            *     8296    35863: contig of 27568 bp in length
            *    35864    35963: gap of unknown length
            *    35964    86799: contig of 50836 bp in length
            *    86800    86899: gap of unknown length
            *    86900   148069: contig of 61170 bp in length.
FEATURES             Location/Qualifiers
     source          1. .148069
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="RP11-36A10"
                     /clone_lib="RPCI human BAC library 11"
ORIGIN

  Query Match             23.1%;  Score 536;  DB 2;  Length 148069;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-296;
  Matches  536;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        376 CAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCA 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16111 CAGAGGAAAATTTGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCA 16052

Qy        436 TTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGAT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16051 TTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAACTTCGACATGGTGAT 15992

Qy        496 AGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGT 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15991 AGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGT 15932

Qy        556 GGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTA 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15931 GGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTA 15872

Qy        616 TGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAA 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15871 TGTTCCAGTATTCCGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAA 15812

Qy        676 TTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAA 735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      15811 TTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAA 15752

Qy        736 CACCATCAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAA 795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15751 CACCATCAAGGAACATTTCACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAA 15692

Qy        796 AGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCC 855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15691 AGCAGAGTTGTGGTTCATTAACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCC 15632

Qy        856 CAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAG 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15631 CAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAG 15576


RESULT 12
AX136632/c
LOCUS       AX136632                 594 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 554 from Patent EP1067182.
ACCESSION   AX136632
VERSION     AX136632.1  GI:14273036
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
            Hayashi,K.
  TITLE     Secretory protein or membrane protein
  JOURNAL   Patent: EP 1067182-A 554 10-JAN-2001;
            Helix Research Institute (JP)
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             20.2%;  Score 468;  DB 6;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-256;
  Matches  468;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1848 TCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 1907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 TCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 409

Qy       1908 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTC 1967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTC 349

Qy       1968 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 2027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 289

Qy       2028 CCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 2087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        288 CCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 229

Qy       2088 ATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTG 2147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 ATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTG 169

Qy       2148 CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 2207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 109

Qy       2208 TCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC 2267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 TCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC 49

Qy       2268 AGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2315
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 AGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 1


RESULT 13
BD123872/c
LOCUS       BD123872                 594 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Secretory protein or membrane protein.
ACCESSION   BD123872
VERSION     BD123872.1  GI:23218817
KEYWORDS    JP 2002017376-A/381.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
            Hayashi,K.
  TITLE     Secretory protein or membrane protein
  JOURNAL   Patent: JP 2002017376-A 381 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002017376-A/381
            PD   22-JAN-2002
            PF   07-JUL-2000 JP 2000253173
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
            PI   SUGIYAMA,
            PI   KOJI HAYASHI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC
            Secretory protein or membrane protein
            FH   Key             Location/Qualifiers
            FT   source          1. .594
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN
```

```
  Query Match             20.2%;  Score 468;  DB 6;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-256;
  Matches  468;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1848 TCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 1907
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 TCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 409

Qy       1908 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTC 1967
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTC 349

Qy       1968 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 2027
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 289

Qy       2028 CCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 2087
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 229

Qy       2088 ATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTG 2147
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 ATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTG 169

Qy       2148 CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 2207
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 109

Qy       2208 TCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC 2267
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 TCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC 49

Qy       2268 AGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 2315
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 AGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC 1


RESULT 14
AC022136
LOCUS       AC022136               125145 bp    DNA     linear   HTG 06-MAY-2000
DEFINITION  Homo sapiens chromosome 5 clone CTD-2221K22, WORKING DRAFT
            SEQUENCE, 37 unordered pieces.
ACCESSION   AC022136
VERSION     AC022136.3  GI:7711710
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 125145)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Human Chromosome 5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 125145)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
```

JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On May 6, 2000 this sequence version replaced gi:7239447.
-------Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 712675
Center clone name: CITB-H1_2221K22

Summary Statistics
Consensus quality: 93614 bases at least Q40
Consensus quality: 109475 bases at least Q30
Consensus quality: 112774 bases at least Q20
Estimated insert size: 97000; pulse field gel estimation
Estimated insert size: 121545; sum-of-contigs estimation
Quality coverage: 5.83 in Q20 bases; pulse field gel estimation
Quality coverage: 4.65 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

*	1	2572: contig of 2572 bp in length
*	2573	2672: gap of unknown length
*	2673	4770: contig of 2098 bp in length
*	4771	4870: gap of unknown length
*	4871	7164: contig of 2294 bp in length
*	7165	7264: gap of unknown length
*	7265	9449: contig of 2185 bp in length
*	9450	9549: gap of unknown length
*	9550	12367: contig of 2818 bp in length
*	12368	12467: gap of unknown length
*	12468	14902: contig of 2435 bp in length
*	14903	15002: gap of unknown length
*	15003	17643: contig of 2641 bp in length
*	17644	17743: gap of unknown length
*	17744	20541: contig of 2798 bp in length
*	20542	20641: gap of unknown length
*	20642	22879: contig of 2238 bp in length
*	22880	22979: gap of unknown length
*	22980	25050: contig of 2071 bp in length
*	25051	25150: gap of unknown length
*	25151	27710: contig of 2560 bp in length
*	27711	27810: gap of unknown length
*	27811	30269: contig of 2459 bp in length
*	30270	30369: gap of unknown length
*	30370	32584: contig of 2215 bp in length
*	32585	32684: gap of unknown length
*	32685	35719: contig of 3035 bp in length
*	35720	35819: gap of unknown length
*	35820	38323: contig of 2504 bp in length

```
            *    38324    38423: gap of unknown length
            *    38424    41441: contig of 3018 bp in length
            *    41442    41541: gap of unknown length
            *    41542    44320: contig of 2779 bp in length
            *    44321    44420: gap of unknown length
            *    44421    47540: contig of 3120 bp in length
            *    47541    47640: gap of unknown length
            *    47641    49926: contig of 2286 bp in length
            *    49927    50026: gap of unknown length
            *    50027    52948: contig of 2922 bp in length
            *    52949    53048: gap of unknown length
            *    53049    55882: contig of 2834 bp in length
            *    55883    55982: gap of unknown length
            *    55983    59431: contig of 3449 bp in length
            *    59432    59531: gap of unknown length
            *    59532    62545: contig of 3014 bp in length
            *    62546    62645: gap of unknown length
            *    62646    65729: contig of 3084 bp in length
            *    65730    65829: gap of unknown length
            *    65830    69494: contig of 3665 bp in length
            *    69495    69594: gap of unknown length
            *    69595    73457: contig of 3863 bp in length
            *    73458    73557: gap of unknown length
            *    73558    76848: contig of 3291 bp in length
            *    76849    76948: gap of unknown length
            *    76949    81440: contig of 4492 bp in length
            *    81441    81540: gap of unknown length
            *    81541    84401: contig of 2861 bp in length
            *    84402    84501: gap of unknown length
            *    84502    87615: contig of 3114 bp in length
            *    87616    87715: gap of unknown length
            *    87716    90814: contig of 3099 bp in length
            *    90815    90914: gap of unknown length
            *    90915    94882: contig of 3968 bp in length
            *    94883    94982: gap of unknown length
            *    94983    99188: contig of 4206 bp in length
            *    99189    99288: gap of unknown length
            *    99289   104355: contig of 5067 bp in length
            *   104356   104455: gap of unknown length
            *   104456   110393: contig of 5938 bp in length
            *   110394   110493: gap of unknown length
            *   110494   116770: contig of 6277 bp in length
            *   116771   116870: gap of unknown length
            *   116871   125145: contig of 8275 bp in length.
FEATURES             Location/Qualifiers
     source          1. .125145
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-2221K22"
                     /clone_lib="CalTech human BAC library D"
ORIGIN

  Query Match             18.2%;  Score 422;  DB 2;  Length 125145;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-230;
  Matches  472;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       1848 TCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 1907
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5002 TCTTTCCAGTCCTCTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTG 5061

Qy       1908 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTC 1967
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5062 TCTCTGAGTGACTTGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTC 5121

Qy       1968 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 2027
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5122 TCATGCGCCTCTCCGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAG 5181

Qy       2028 CCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 2087
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5182 CCTCTCTCACTCCTGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGC 5241

Qy       2088 ATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTG 2147
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5242 ATATTCTTTCAGTTTCTGTTTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTG 5301

Qy       2148 CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 2207
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5302 CCCTGTGCTTGAGAGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTG 5361

Qy       2208 TCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCC 2267
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       5362 TCTCTGGTGCCCACAGTGAGCTCCTTCTTGGCTGAGCAGGCTTGGAGACTGTAGGTTTCC 5421

Qy       2268 AGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5422 AGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 5474
```

```
RESULT 15
AR541778
LOCUS       AR541778                2426 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 26 from patent US 6743619.
ACCESSION   AR541778
VERSION     AR541778.1  GI:53933858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Tang,Y.T., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Ren,F.,
            Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,J.-R.,
            Wang,D. and Drmanac,R.T.
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: US 6743619-A 26 01-JUN-2004;
FEATURES             Location/Qualifiers
     source          1. .2426
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             9.9%;  Score 230;  DB 6;  Length 2426;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.2e-119;
  Matches  230;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2047 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGT 2106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGT 60

Qy       2107 TTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCA 2166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCA 120

Qy       2167 GGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGA 2226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCACAGTGA 180

Qy       2227 GCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCT 2276
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCCT 230


Search completed: March 25, 2005, 14:36:45
Job time : 9908 secs
```

GenCore version 5.1.6
Run on: March 25, 2005, 08:49:37 ; Search time 1161 Seconds
(without alignments)
11829.285 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 agggtcccttagccgggcgc.....tctctccccaacctcactaa 2320
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description

RESULT 1
ID AAC58107 standard; cDNA; 2320 BP.
DE Human PRO1780 nucleotide sequence SEQ ID NO:12.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 3; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 2
ID AAA37101 standard; cDNA; 2320 BP.
DE Human PRO1780 (UNQ842) cDNA sequence SEQ ID NO:281.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 3; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 3
ID AAF54401 standard; DNA; 2320 BP.
DE Primer #82 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 4; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 4

ID ACD68440 standard; cDNA; 2320 BP.
DE Novel human secreted and transmembrane protein PRO1780 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 9; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 5
ID ACH04542 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 9; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 6
ID ACD68086 standard; cDNA; 2320 BP.
DE Novel human secreted and transmembrane protein PRO1780 cDNA.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 9; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 7
ID ADC18150 standard; cDNA; 2320 BP.
DE Human PRO polynucleotide #80.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 10; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 8
ID ADD70796 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 10; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 9
ID ADD39873 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 10; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 10
ID ADD70319 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 10; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 11
ID ADD38440 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 12
ID ADD39396 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 13
ID ADD38919 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ADD40350 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ADE50571 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ADE20183 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ADE50094 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ADE21652 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 10; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ADF30077 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 10; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ADF55970 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 10; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ADH99474 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 10; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID ADE96654 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 12; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ADF25965 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 12; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ADF24864 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 2320; DB 12; Length 2320;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ADF29600 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003203401-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ADE97131 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ADH03169 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ADH04123 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ADH03646 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ADH04600 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ADH61601 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ADL94800 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2004073015-A1.
PD 15-APR-2004.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID AAF93775 standard; cDNA; 2341 BP.
DE Human cDNA encoding a membrane or secretory protein clone PSEC0073.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 93.2%; Score 2162; DB 5; Length 2341;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 34
ID AAL41485 standard; DNA; 2944 BP.
DE Drug metabolising enzyme encoding DNA - 7486594CB1.
PN WO200266654-A2.
PD 29-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 84.4%; Score 1957; DB 6; Length 2944;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 35
ID AAS62475 standard; cDNA; 2074 BP.
DE cDNA sequence #262 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 74.0%; Score 1717; DB 6; Length 2074;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 36
ID ADR19692 standard; DNA; 2263 BP.
DE Human drug metabolising enzyme (DME)-13 gene sequence.
PN WO200226988-A2.
PD 04-APR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 33.4%; Score 776; DB 7; Length 2263;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 37
ID ABA09537 standard; cDNA; 1898 BP.
DE Human PRO1780 homologue-encoding cDNA, SEQ ID NO:1313.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.5%; Score 591; DB 4; Length 1898;
Best Local Similarity 99.8%; Pred. No. 9.5e-282;
RESULT 38
ID AAS81804 standard; cDNA; 2220 BP.
DE DNA encoding novel human diagnostic protein #17608.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 20.9%; Score 484; DB 5; Length 2220;
Best Local Similarity 100.0%; Pred. No. 9.9e-229;
RESULT 39
ID AAF94120 standard; DNA; 594 BP.
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 554.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.

Query Match 20.2%; Score 468; DB 5; Length 594;
Best Local Similarity 100.0%; Pred. No. 8e-221;

RESULT 40
ID ADN39359 standard; cDNA; 923 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B43.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 19.0%; Score 441; DB 11; Length 923;
Best Local Similarity 100.0%; Pred. No. 1.9e-207;

RESULT 41
ID AAS84832 standard; cDNA; 2721 BP.
DE DNA encoding novel human diagnostic protein #20636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 17.5%; Score 407; DB 5; Length 2721;
Best Local Similarity 100.0%; Pred. No. 1.4e-190;

RESULT 42
ID ABX70800 standard; cDNA; 2426 BP.
DE Novel human cDNA sequence #25.
PN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match 9.9%; Score 230; DB 8; Length 2426;
Best Local Similarity 100.0%; Pred. No. 7e-103;

RESULT 43
ID AAS84831 standard; cDNA; 1242 BP.
DE DNA encoding novel human diagnostic protein #20635.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.7%; Score 224; DB 5; Length 1242;
Best Local Similarity 100.0%; Pred. No. 6.5e-100;

RESULT 44
ID AAS82074 standard; cDNA; 1242 BP.
DE DNA encoding novel human diagnostic protein #17878.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.7%; Score 224; DB 5; Length 1242;
Best Local Similarity 100.0%; Pred. No. 6.5e-100;

RESULT 45
ID AAF93971 standard; DNA; 770 BP.
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 405.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.0%; Score 139; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 8.3e-58;

RESULT 46
ID AAS81803 standard; cDNA; 659 BP.
DE DNA encoding novel human diagnostic protein #17607.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 2.9%; Score 68; DB 5; Length 659;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;

RESULT 47
ID ABL57725 standard; DNA; 1182 BP.
DE Human sbg10054OUDPGT gene #1.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 2.9%; Score 68; DB 6; Length 1182;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;

RESULT 48
ID ABL57726 standard; DNA; 1572 BP.
DE Human sbg10054OUDPGT gene #2.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 2.9%; Score 68; DB 6; Length 1572;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;

RESULT 49
ID ABK90831 standard; cDNA; 1851 BP.
DE cDNA encoding drug metabolising enzyme.
PN US2002082194-A1.
PD 27-JUN-2002.
PA (GUEG/) GUEGLER K.
PA (WEBS/) WEBSTER M.
PA (YANC/) YAN C.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.9%; Score 68; DB 6; Length 1851;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;

RESULT 50
ID AAD24667 standard; cDNA; 2086 BP.
DE Human drug metabolising enzyme (DME)-2 cDNA.
PN WO200179468-A2.
PD 25-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.9%; Score 68; DB 6; Length 2086;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;

RESULT 51
ID ADA21188 standard; cDNA; 2268 BP.
DE Human secreted protein SECP-42 encoding cDNA SEQ ID NO:93.
PN WO2003068943-A2.
PD 21-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.9%; Score 68; DB 9; Length 2268;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;

RESULT 52
ID ADQ75567 standard; cDNA; 2791 BP.
DE Uridine diphosphate-galactosyl ceramide glucuronyl collagen transferase.
PN CN1380409-A.
PD 20-NOV-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 2.9%; Score 68; DB 11; Length 2791;

Best Local Similarity 100.0%; Pred. No. 1.3e-22;
RESULT 53
ID AAD06821 standard; cDNA; 2797 BP.
DE Human secreted protein Zalpha37 cDNA.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 2.9%; Score 68; DB 4; Length 2797;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
RESULT 54
ID ADA53720 standard; cDNA; 2823 BP.
DE Human coding sequence, SEQ ID 1288.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.9%; Score 68; DB 10; Length 2823;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
RESULT 55
ID ADQ64368 standard; cDNA; 5002 BP.
DE Novel human cDNA sequence #1529.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.9%; Score 68; DB 12; Length 5002;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
RESULT 56
ID ABK90832 standard; DNA; 42999 BP.
DE Genomic DNA encoding drug metabolising enzyme.
PN US2002082194-A1.
PD 27-JUN-2002.
PA (GUEG/) GUEGLER K.
PA (WEBS/) WEBSTER M.
PA (YANC/) YAN C.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.9%; Score 68; DB 6; Length 42999;
Best Local Similarity 100.0%; Pred. No. 1.4e-22;
RESULT 57
ID AAD25345 standard; cDNA; 2082 BP.
DE Human UDP-glycosyltransferase, 32626 cDNA.
PN WO200202774-A2.
PD 10-JAN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.4%; Score 55; DB 6; Length 2082;
Best Local Similarity 100.0%; Pred. No. 3.6e-16;
RESULT 58
ID ADN02571 standard; DNA; 2868 BP.
DE Human hepatouracil dinucleotide glycosyltransferase 29.7 DNA.
PN CN1393551-A.
PD 29-JAN-2003.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match 2.4%; Score 55; DB 11; Length 2868;
Best Local Similarity 100.0%; Pred. No. 3.6e-16;
RESULT 59
ID ADB62657 standard; cDNA; 1842 BP.
DE Human cDNA encoding clone KIDNE20186170.

PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.2%; Score 52; DB 10; Length 1842;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
RESULT 60
ID AAC58024 standard; DNA; 45 BP.
DE Human PRO1780 hybridisation probe SEQ ID NO:16.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 61
ID AAA37270 standard; DNA; 45 BP.
DE Human PRO1780 hybridisation probe SEQ ID NO:285.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 62
ID AAF54404 standard; DNA; 45 BP.
DE Primer #83 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 63
ID ACD68443 standard; DNA; 45 BP.
DE Novel human secreted and transmembrane protein related probe #41.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 64
ID ACH04545 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 65
ID ACD68089 standard; DNA; 45 BP.
DE Novel human secreted and transmembrane protein related probe #41.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 66
ID ADC18154 standard; DNA; 45 BP.
DE Human PRO probe #41.

PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 67
ID ADD70800 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 68
ID ADD39877 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 69
ID ADD70323 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 70
ID ADD38444 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 71
ID ADD39400 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 72
ID ADD38923 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 73
ID ADD40354 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003082627-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 74
ID ADE50575 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 75
ID ADE20187 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 76
ID ADE50098 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 77
ID ADE21656 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 78
ID ADF30081 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 79
ID ADF55974 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 80
ID ADH99478 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003065142-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 81
ID ADE96658 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 82
ID ADF25969 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 83
ID ADF24868 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 84
ID ADF29604 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 85
ID ADE97135 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 86
ID ADH03173 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 87
ID ADH04127 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 88
ID ADH03650 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 89
ID ADH04604 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 90
ID ADH61605 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 91
ID ADL94804 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
RESULT 92
ID AAL05664 standard; DNA; 5973 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8352.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.9%; Score 45; DB 4; Length 5973;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
RESULT 93
ID AAL05665 standard; DNA; 5974 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8353.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.9%; Score 45; DB 4; Length 5974;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
RESULT 94
ID ACN45086 standard; DNA; 54493 BP.
DE Human genomic sequence hCG37578.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.3%; Score 30; DB 11; Length 54493;

Best Local Similarity 100.0%; Pred. No. 0.00097;
RESULT 95
ID AAK24438 standard; DNA; 277 BP.
DE Human brain expressed single exon probe SEQ ID NO: 24429.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.2%; Score 29; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 0.0026;
RESULT 96
ID AAK11854 standard; DNA; 507 BP.
DE Human brain expressed single exon probe SEQ ID NO: 11845.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.2%; Score 29; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0.0026;
RESULT 97
ID AAS41046 standard; cDNA; 923 BP.
DE cDNA encoding novel human enzyme polypeptide #262.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.2%; Score 29; DB 4; Length 923;
Best Local Similarity 100.0%; Pred. No. 0.0027;
RESULT 98
ID AAS41586 standard; cDNA; 981 BP.
DE cDNA encoding novel human enzyme polypeptide #802.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.2%; Score 29; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 0.0027;
RESULT 99
ID AAL01667 standard; cDNA; 981 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 1668.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.2%; Score 29; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 0.0027;
RESULT 100
ID AAL05663 standard; DNA; 2751 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8351.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.2%; Score 29; DB 4; Length 2751;
Best Local Similarity 100.0%; Pred. No. 0.0028;
RESULT 101
ID AAD06823 standard; cDNA; 2212 BP.
DE Mouse secreted protein Zalpha37 cDNA.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.1%; Score 26; DB 4; Length 2212;
Best Local Similarity 100.0%; Pred. No. 0.084;

RESULT 102
ID AAC58023 standard; DNA; 24 BP.
DE Human PRO1780 reverse PCR primer SEQ ID NO:15.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 3; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 103
ID AAC58022 standard; DNA; 24 BP.
DE Human PRO1780 forward PCR primer SEQ ID NO:14.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 3; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 104
ID AAA37269 standard; DNA; 24 BP.
DE Human PRO1780 reverse PCR primer SEQ ID NO:284.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 3; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 105
ID AAA37268 standard; DNA; 24 BP.
DE Human PRO1780 forward PCR primer SEQ ID NO:283.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 3; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 106
ID AAF54403 standard; DNA; 24 BP.
DE DNA encoding protein of the invention #80.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 4; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 107
ID AAF54402 standard; DNA; 24 BP.
DE Probe #41 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 4; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 108
ID AAD06829 standard; DNA; 24 BP.
DE Human secreted protein Zalpha37 DNA amplifying primer ZC25939.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
  Query Match 1.0%; Score 24; DB 4; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 109

ID ACD68441 standard; DNA; 24 BP.
DE Novel human secreted and transmembrane protein related primer #81.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 9; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 110
ID ACD68442 standard; DNA; 24 BP.
DE Novel human secreted and transmembrane protein related primer #82.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 9; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 111
ID ACH04544 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 9; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 112
ID ACH04543 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 9; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 113
ID ACD68087 standard; DNA; 24 BP.
DE Novel human secreted and transmembrane protein related primer #81.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 9; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 114
ID ACD68088 standard; DNA; 24 BP.
DE Novel human secreted and transmembrane protein related primer #82.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 9; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 115
ID ADC18152 standard; DNA; 24 BP.
DE Human PRO PCR primer #81.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 10; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 116
ID ADC18153 standard; DNA; 24 BP.

DE Human PRO PCR primer #82.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 117
ID ADD70798 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 118
ID ADD70799 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 119
ID ADD39875 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 120
ID ADD39876 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 121
ID ADD70322 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 122
ID ADD70321 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 123
ID ADD38442 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.

PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 124
ID ADD38443 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 125
ID ADD39399 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 126
ID ADD39398 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 127
ID ADD38922 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 128
ID ADD38921 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 129
ID ADD40352 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 130
ID ADD40353 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003082627-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 131
ID ADE50574 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 132
ID ADE50573 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 133
ID ADE20186 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 134
ID ADE20185 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 135
ID ADE50096 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 136
ID ADE50097 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 137
ID ADE21655 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003082628-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 138
ID ADE21654 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 139
ID ADF30080 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 140
ID ADF30079 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 141
ID ADF55973 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 142
ID ADF55972 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 143
ID ADH99476 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 144
ID ADH99477 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 1.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 145
ID ADE96657 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 146
ID ADE96656 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 147
ID ADF25967 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 148
ID ADF25968 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 149
ID ADF24866 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 150
ID ADF24867 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.71;

RESULT 151
ID ADF29603 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 24; DB 12; Length 24;

  Best Local Similarity   100.0%; Pred. No. 0.71;
RESULT 152
ID   ADF29602 standard; DNA; 24 BP.
DE   Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN   US2003203401-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity   100.0%; Pred. No. 0.71;
RESULT 153
ID   ADE97134 standard; DNA; 24 BP.
DE   Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN   US2003195334-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity   100.0%; Pred. No. 0.71;
RESULT 154
ID   ADE97133 standard; DNA; 24 BP.
DE   Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN   US2003195334-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
  Query Match   1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity   100.0%; Pred. No. 0.71;
RESULT 155
ID   ADH03172 standard; DNA; 24 BP.
DE   Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN   US2003216562-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
  Query Match   1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity   100.0%; Pred. No. 0.71;
RESULT 156
ID   ADH03171 standard; DNA; 24 BP.
DE   Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN   US2003216562-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
  Query Match   1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity   100.0%; Pred. No. 0.71;
RESULT 157
ID   ADH04125 standard; DNA; 24 BP.
DE   Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN   US2003220471-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
  Query Match   1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity   100.0%; Pred. No. 0.71;
RESULT 158
ID   ADH04126 standard; DNA; 24 BP.
DE   Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN   US2003220471-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
  Query Match   1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity   100.0%; Pred. No. 0.71;

RESULT 159
ID ADH03649 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 160
ID ADH03648 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 161
ID ADH04603 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 162
ID ADH04602 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 163
ID ADH61604 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 164
ID ADH61603 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 165
ID ADL94803 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #2.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 166

ID ADL94802 standard; DNA; 24 BP.
DE Human secreted/transmembrane protein PRO1780 PCR primer #1.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 24; DB 12; Length 24;
  Best Local Similarity 100.0%; Pred. No. 0.71;
RESULT 167
ID AAC58051 standard; DNA; 23 BP.
DE Human PRO1780 reverse PCR primer SEQ ID NO:73.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 3; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 168
ID AAF54531 standard; DNA; 23 BP.
DE Primer #137 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 4; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 169
ID ACD68570 standard; DNA; 23 BP.
DE Novel human secreted and transmembrane protein related primer #142.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 9; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 170
ID ACH04672 standard; DNA; 23 BP.
DE Human secreted/transmembrane protein PRO1780 Taqman PCR primer #2.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 9; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 171
ID ACD68216 standard; DNA; 23 BP.
DE Novel human secreted and transmembrane protein related primer #142.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 9; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 172
ID ADC18324 standard; DNA; 23 BP.
DE Human PRO PCR primer #139.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 10; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 173
ID ADD70970 standard; DNA; 23 BP.

DE Human PRO 1780 Taqman PCR primer #2.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 174
ID ADD40047 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 175
ID ADD70493 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 176
ID ADD38614 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 177
ID ADD39570 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 178
ID ADD39093 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 179
ID ADD40524 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 180
ID ADE50745 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.

PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 10; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 181
ID ADE20357 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 10; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 182
ID ADE50268 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 10; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 183
ID ADE21826 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 10; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 184
ID ADF30251 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 10; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 185
ID ADF56144 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 10; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 186
ID ADH99648 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 1.0%; Score 23; DB 10; Length 23;
  Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 187
ID ADE96828 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003195347-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 188
ID ADF26139 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 189
ID ADF25038 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 190
ID ADF29774 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 191
ID ADE97305 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 192
ID ADH03343 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 193
ID ADH04297 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 194
ID ADH03820 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2003224478-A1.
PD 04-DEC-2003.

PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 195
ID ADH04774 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 196
ID ADH61775 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 197
ID ADL94974 standard; DNA; 23 BP.
DE Human PRO 1780 Taqman PCR primer #2.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2;
RESULT 198
ID ADQ57767 standard; DNA; 582 BP.
DE Novel canine microarray-related DNA sequence SeqID9069.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
Query Match 1.0%; Score 23; DB 13; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.5;
RESULT 199
ID ACN45084 standard; DNA; 49753 BP.
DE Mouse genomic sequence mCG7831.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.0%; Score 23; DB 11; Length 49753;
Best Local Similarity 100.0%; Pred. No. 2.8;
RESULT 200
ID ACH94527 standard; DNA; 582 BP.
DE Klebsiella pneumoniae polynucleotide seqid 322.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 0.9%; Score 22; DB 11; Length 582;
Best Local Similarity 100.0%; Pred. No. 7.7;
RESULT 201
ID ACH94551 standard; DNA; 582 BP.
DE Klebsiella pneumoniae polynucleotide seqid 346.
PN US6610836-B1.
PD 26-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 0.9%; Score 22; DB 11; Length 582;
Best Local Similarity 100.0%; Pred. No. 7.7;
RESULT 202
ID ADA19261 standard; cDNA; 1753 BP.
DE Human insulin resistance marker IRM90 (DJ159A19.3) cDNA.
PN WO200298355-A2.
PD 12-DEC-2002.
PA (CLIN-) CLINGENIX INC.
Query Match 0.9%; Score 22; DB 10; Length 1753;
Best Local Similarity 100.0%; Pred. No. 8;
RESULT 203
ID ADQ63954 standard; cDNA; 2661 BP.
DE Novel human cDNA sequence #1115.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 0.9%; Score 22; DB 12; Length 2661;
Best Local Similarity 100.0%; Pred. No. 8.1;
RESULT 204
ID AAD31108 standard; cDNA; 6236 BP.
DE Human transcription factor and zinc finger protein (TFZN)-8 cDNA.
PN WO200224895-A2.
PD 28-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 0.9%; Score 22; DB 6; Length 6236;
Best Local Similarity 100.0%; Pred. No. 8.3;
RESULT 205
ID AAC58050 standard; DNA; 21 BP.
DE Human PRO1780 hybridisation probe SEQ ID NO:72.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 206
ID AAF54530 standard; DNA; 21 BP.
DE Probe #67 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 207
ID ACD68569 standard; DNA; 21 BP.
DE Novel human secreted and transmembrane protein related probe #63.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 208
ID ACH04671 standard; DNA; 21 BP.
DE Human secreted/transmembrane protein PRO1780 Taqman PCR probe.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

```
  Query Match             0.9%;  Score 21;  DB 9;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 22;
RESULT 209
ID   ACD68215 standard; DNA; 21 BP.
DE   Novel human secreted and transmembrane protein related probe #63.
PN   US2003073129-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.9%;  Score 21;  DB 9;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 22;
RESULT 210
ID   ADC18323 standard; DNA; 21 BP.
DE   Human PRO probe #68.
PN   US2003064925-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.9%;  Score 21;  DB 10;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 22;
RESULT 211
ID   ADD70969 standard; DNA; 21 BP.
DE   Human PRO 1780 Taqman PCR probe.
PN   US2003099625-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.9%;  Score 21;  DB 10;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 22;
RESULT 212
ID   ADD40046 standard; DNA; 21 BP.
DE   Human PRO 1780 Taqman PCR probe.
PN   US2003083462-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.9%;  Score 21;  DB 10;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 22;
RESULT 213
ID   ADD70492 standard; DNA; 21 BP.
DE   Human PRO 1780 Taqman PCR probe.
PN   US2003054406-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.9%;  Score 21;  DB 10;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 22;
RESULT 214
ID   ADD38613 standard; DNA; 21 BP.
DE   Human PRO 1780 Taqman PCR probe.
PN   US2003096955-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.9%;  Score 21;  DB 10;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 22;
RESULT 215
ID   ADD39569 standard; DNA; 21 BP.
DE   Human PRO 1780 Taqman PCR probe.
PN   US2003096954-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.9%;  Score 21;  DB 10;  Length 21;
```

Best Local Similarity 100.0%; Pred. No. 22;
RESULT 216
ID ADD39092 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 217
ID ADD40523 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 218
ID ADE50744 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 219
ID ADE20356 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 220
ID ADE50267 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 221
ID ADE21825 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 222
ID ADF30250 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 0.9%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;

RESULT 223
ID ADF56143 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 10; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 224
ID ADH99647 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 10; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 225
ID ADE96827 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 226
ID ADF26138 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 227
ID ADF25037 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 228
ID ADF29773 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 229
ID ADE97304 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 230

ID ADH03342 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 231
ID ADH04296 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 232
ID ADH03819 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 233
ID ADH04773 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 234
ID ADH61774 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 235
ID ADL94973 standard; DNA; 21 BP.
DE Human PRO 1780 Taqman PCR probe.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
  Query Match 0.9%; Score 21; DB 12; Length 21;
  Best Local Similarity 100.0%; Pred. No. 22;
RESULT 236
ID ABA12900 standard; cDNA; 328 BP.
DE Human nervous system related polynucleotide SEQ ID NO 1907.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.9%; Score 20; DB 5; Length 328;
  Best Local Similarity 100.0%; Pred. No. 74;
RESULT 237
ID ACF71876 standard; DNA; 369 BP.

DE Photorhabdus luminescens nucleotide sequence #10343.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 0.9%; Score 20; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 74;
RESULT 238
ID ABA18507 standard; DNA; 401 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10838.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.9%; Score 20; DB 5; Length 401;
Best Local Similarity 100.0%; Pred. No. 75;
RESULT 239
ID ACH33594 standard; cDNA; 465 BP.
DE Human endothelial cell cDNA #1727.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 0.9%; Score 20; DB 9; Length 465;
Best Local Similarity 100.0%; Pred. No. 75;
RESULT 240
ID ADS50876 standard; cDNA; 654 BP.
DE Bacterial polynucleotide #5619.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 0.9%; Score 20; DB 13; Length 654;
Best Local Similarity 100.0%; Pred. No. 76;
RESULT 241
ID ABZ80029 standard; cDNA; 3339 BP.
DE Arabidopsis thaliana phytochrome E encoding cDNA SEQ ID NO:1.
PN WO2003015500-A2.
PD 27-FEB-2003.
PA (PARA-) PARADIGM GENETICS INC.
Query Match 0.9%; Score 20; DB 10; Length 3339;
Best Local Similarity 100.0%; Pred. No. 80;
RESULT 242
ID ADL27164 standard; DNA; 87761 BP.
DE Human genomic sequence for hCG23764.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 0.9%; Score 20; DB 11; Length 87761;
Best Local Similarity 100.0%; Pred. No. 89;
RESULT 243

ID ADA03086 standard; DNA; 94529 BP.
DE Human hCG23764 carcinoma associated gene, SEQ ID NO:1604.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
  Query Match 0.9%; Score 20; DB 9; Length 94529;
  Best Local Similarity 100.0%; Pred. No. 89;
RESULT 244
ID ADB72824 standard; DNA; 94529 BP.
DE Human hCG23764 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
  Query Match 0.9%; Score 20; DB 10; Length 94529;
  Best Local Similarity 100.0%; Pred. No. 89;
RESULT 245
ID ADA66370 standard; DNA; 94531 BP.
DE Human hCG23764 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
  Query Match 0.9%; Score 20; DB 9; Length 94531;
  Best Local Similarity 100.0%; Pred. No. 89;
RESULT 246
  Query Match 0.9%; Score 20; DB 10; Length 110000;
  Best Local Similarity 100.0%; Pred. No. 89;
RESULT 247
  Query Match 0.9%; Score 20; DB 10; Length 110000;
  Best Local Similarity 100.0%; Pred. No. 89;
RESULT 248
  Query Match 0.9%; Score 20; DB 10; Length 110000;
  Best Local Similarity 100.0%; Pred. No. 89;
RESULT 249
  Query Match 0.9%; Score 20; DB 13; Length 110000;
  Best Local Similarity 100.0%; Pred. No. 89;
RESULT 250
ID ADQ97397 standard; DNA; 225587 BP.
DE Human cancer associated sequence HD08-043, SEQ ID 374.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
  Query Match 0.9%; Score 20; DB 12; Length 225587;
  Best Local Similarity 100.0%; Pred. No. 91;
RESULT 251
ID ADJ11817 standard; DNA; 393 BP.
DE Rice cDNA modulated by post-transcriptional gene silencing SeqID 453.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 0.8%; Score 19; DB 11; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
RESULT 252
ID ADJ11485 standard; DNA; 396 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 121.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 0.8%; Score 19; DB 11; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
RESULT 253
ID ACH35408 standard; cDNA; 496 BP.
DE Human endothelial cell cDNA #3541.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 0.8%; Score 19; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
RESULT 254
ID AAZ50416 standard; cDNA; 516 BP.
DE Vernonia transcription coactivator PC4(P15) type 1 cDNA.
PN WO200005377-A2.
PD 03-FEB-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 0.8%; Score 19; DB 3; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 255
ID AAL25083 standard; cDNA; 674 BP.
DE Human breast cancer expressed polynucleotide 17540.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 0.8%; Score 19; DB 4; Length 674;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 256
ID AAF44940 standard; cDNA; 719 BP.
DE Human breast cancer related protein coding sequence SEQ ID NO: 96.
PN WO200078960-A2.
PD 28-DEC-2000.

PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 19; DB 4; Length 719;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 257
ID ACF67756 standard; DNA; 1206 BP.
DE Photorhabdus luminescens nucleotide sequence #6223.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 0.8%; Score 19; DB 10; Length 1206;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 258
ID ADM91973 standard; DNA; 1212 BP.
DE S pneumoniae antigenic protein-encoding gene sequence SeqID170.
PN WO2004020609-A2.
PD 11-MAR-2004.
PA (TUFT) UNIV TUFTS.
Query Match 0.8%; Score 19; DB 12; Length 1212;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 259
ID ABX07539 standard; DNA; 1218 BP.
DE S. pneumoniae type 4 strain coding region #1827.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 0.8%; Score 19; DB 10; Length 1218;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 260
ID ACN43573 standard; cDNA; 1560 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2448.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 0.8%; Score 19; DB 13; Length 1560;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 261
ID ADI43442 standard; DNA; 1563 BP.
DE Plant transcription factor polynucleotide #1304.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.

Query Match 0.8%; Score 19; DB 12; Length 1563;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

RESULT 262
ID ABZ16704 standard; DNA; 1856 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4509.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 0.8%; Score 19; DB 6; Length 1856;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 263
ID ABZ14955 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2760.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 0.8%; Score 19; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 264
ID AAZ52471 standard; DNA; 2206 BP.
DE HTRM clone 3279329 DNA sequence.
PN WO9957144-A2.
PD 11-NOV-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 0.8%; Score 19; DB 3; Length 2206;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 265
ID ADA13370 standard; cDNA; 2238 BP.
DE Human intracellular signalling molecule INTSIG-7 cDNA, SEQ ID NO:52.
PN WO2003031568-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 0.8%; Score 19; DB 10; Length 2238;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 266
ID AAH15056 standard; cDNA; 2309 BP.
DE Human cDNA sequence SEQ ID NO:13052.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 0.8%; Score 19; DB 4; Length 2309;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 267
ID ADQ18551 standard; DNA; 2309 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1370.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 0.8%; Score 19; DB 12; Length 2309;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 268
ID ABZ11549 standard; cDNA; 2408 BP.
DE Human polynucleotide SEQ ID NO 431.
PN WO200270539-A2.
PD 12-SEP-2002.

PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 19; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 269
ID ADM44067 standard; cDNA; 2408 BP.
DE Novel human arginine-rich protein cDNA #431.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Query Match 0.8%; Score 19; DB 12; Length 2408;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 270
ID ABK49449 standard; cDNA; 2424 BP.
DE cDNA encoding human transporter protein.
PN WO200224749-A2.
PD 28-MAR-2002.
PA (PEKE) PE CORP NY.
Query Match 0.8%; Score 19; DB 6; Length 2424;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 271
ID ABL40302 standard; cDNA; 2628 BP.
DE Human TLCC-3 cDNA (coding region only).
PN WO200200718-A2.
PD 03-JAN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 0.8%; Score 19; DB 6; Length 2628;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 272
ID ADQ85330 standard; cDNA; 2678 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2144.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 0.8%; Score 19; DB 12; Length 2678;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 273
ID AAV07912 standard; DNA; 2699 BP.
DE Helicobacter pylori 76 kDa polypeptide GHPO 789 DNA.
PN WO9843479-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 19; DB 2; Length 2699;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 274
ID AAD61566 standard; DNA; 2699 BP.
DE Helicobacter pylori p76 antigen DNA #2.
PN US6576244-B1.
PD 10-JUN-2003.
PA (ACAM-) ACAMBIS INC.
Query Match 0.8%; Score 19; DB 10; Length 2699;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 275

ID ABL40301 standard; cDNA; 2724 BP.
DE Human TLCC-3 cDNA.
PN WO200200718-A2.
PD 03-JAN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
  Query Match 0.8%; Score 19; DB 6; Length 2724;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 276
ID AAF22401 standard; cDNA; 2793 BP.
DE Human secreted protein gene 29 SEQ ID NO:39.
PN WO200061629-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
  Query Match 0.8%; Score 19; DB 3; Length 2793;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 277
ID ABZ73691 standard; cDNA; 2793 BP.
DE Secreted protein-encoding gene 388 cDNA clone HPJBJ51, SEQ ID NO:421.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 19; DB 8; Length 2793;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 278
ID ABZ67290 standard; cDNA; 2793 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 410.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 19; DB 10; Length 2793;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 279
ID AAS02554 standard; cDNA; 2795 BP.
DE Human secreted protein gene #35.
PN WO200123409-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 19; DB 4; Length 2795;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 280
ID ABZ73668 standard; cDNA; 2795 BP.
DE Secreted protein-encoding gene 388 cDNA clone HPJBJ51, SEQ ID NO:398.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 19; DB 8; Length 2795;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 281
ID ABZ67265 standard; cDNA; 2795 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 385.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 19; DB 10; Length 2795;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 282

ID AAV72001 standard; DNA; 2798 BP.
DE Helicobacter pylori 76 kDa polypeptide GHPO 386 DNA.
PN WO9843479-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 19; DB 2; Length 2798;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 283
ID AAD61565 standard; DNA; 2798 BP.
DE Helicobacter pylori p76 antigen DNA #1.
PN US6576244-B1.
PD 10-JUN-2003.
PA (ACAM-) ACAMBIS INC.
  Query Match 0.8%; Score 19; DB 10; Length 2798;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 284
ID ABZ11477 standard; cDNA; 2816 BP.
DE Human polynucleotide SEQ ID NO 359.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
  Query Match 0.8%; Score 19; DB 6; Length 2816;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 285
ID ABZ11958 standard; cDNA; 2816 BP.
DE Human polynucleotide SEQ ID NO 840.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
  Query Match 0.8%; Score 19; DB 6; Length 2816;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 286
ID ABX04986 standard; cDNA; 2816 BP.
DE Human novel polynucleotide #1.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
  Query Match 0.8%; Score 19; DB 8; Length 2816;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 287
ID ADM44476 standard; cDNA; 2816 BP.
DE Novel human arginine-rich protein cDNA #840.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
  Query Match 0.8%; Score 19; DB 12; Length 2816;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 288
ID ADM43995 standard; cDNA; 2816 BP.
DE Novel human arginine-rich protein cDNA #359.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.

PA (DRMA/) DRMANAC R T.
Query Match 0.8%; Score 19; DB 12; Length 2816;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 289
ID ADQ63624 standard; cDNA; 2954 BP.
DE Novel human cDNA sequence #785.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 0.8%; Score 19; DB 12; Length 2954;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 290
ID AAV44295 standard; cDNA; 3550 BP.
DE Human secreted protein clone CJ145_1 cDNA.
PN WO9827205-A2.
PD 25-JUN-1998.
PA (GEMY) GENETICS INST INC.
Query Match 0.8%; Score 19; DB 2; Length 3550;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 291
ID AAF98469 standard; cDNA; 3550 BP.
DE Human cDNA clone CJ145_1 sequence SEQ ID 160.
PN WO200119988-A1.
PD 22-MAR-2001.
PA (GEMY) GENETICS INST INC.
Query Match 0.8%; Score 19; DB 5; Length 3550;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 292
ID ADQ23023 standard; DNA; 4046 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5843.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 0.8%; Score 19; DB 12; Length 4046;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 293
ID ACN40547 standard; cDNA; 4282 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326649, SEQ ID NO:5391.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 19; DB 13; Length 4282;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 294
ID AAI58667 standard; cDNA; 4352 BP.
DE Human polynucleotide SEQ ID NO 870.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 19; DB 4; Length 4352;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 295
ID ADQ98885 standard; cDNA; 4352 BP.
DE DNA encoding human GPCR-like protein seqid 555.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.

Query Match 0.8%; Score 19; DB 5; Length 4352;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 296
ID ADB48645 standard; cDNA; 4352 BP.
DE Novel human cDNA SEQ ID NO 555.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match 0.8%; Score 19; DB 9; Length 4352;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 297
ID AAI60453 standard; cDNA; 4377 BP.
DE Human polynucleotide SEQ ID NO 4442.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 19; DB 4; Length 4377;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

RESULT 298
ID ACN45184 standard; DNA; 26533 BP.
DE Mouse genomic sequence mCG9336.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 0.8%; Score 19; DB 11; Length 26533;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;

RESULT 299
ID AAV52204 standard; DNA; 32768 BP.
DE Streptococcus pneumoniae genome fragment SEQ ID NO:71.
PN WO9818931-A2.
PD 07-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 19; DB 2; Length 32768;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;

RESULT 300
ID ACN44896 standard; DNA; 40568 BP.
DE Mouse genomic sequence mCG54271.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 0.8%; Score 19; DB 11; Length 40568;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;

RESULT 301
ID AAX23518 standard; DNA; 49998 BP.
DE Human kidney aminopeptidase P genomic DNA fragment 2.
PN WO9911799-A2.
PD 11-MAR-1999.
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.
Query Match 0.8%; Score 19; DB 2; Length 49998;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;

RESULT 302
ID ABD33295 standard; DNA; 64125 BP.
DE Human cancer-associated (CA) gene HD07-052.

PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
  Query Match 0.8%; Score 19; DB 13; Length 64125;
  Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 303
ID ACN44320 standard; DNA; 77941 BP.
DE Mouse genomic sequence mCG17383.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
  Query Match 0.8%; Score 19; DB 11; Length 77941;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 304
ID ACN37242 standard; DNA; 78294 BP.
DE Human periodontal disease related gene PTGER3 SEQ ID NO:152.
  Query Match 0.8%; Score 19; DB 13; Length 78294;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 305
ID ADQ59189 standard; DNA; 81679 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:26.
PN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
  Query Match 0.8%; Score 19; DB 12; Length 81679;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 306
ID ADQ97298 standard; DNA; 95484 BP.
DE Mouse cancer associated sequence MD08-028, SEQ ID 275.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
  Query Match 0.8%; Score 19; DB 12; Length 95484;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 307
  Query Match 0.8%; Score 19; DB 2; Length 110000;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 308
  Query Match 0.8%; Score 19; DB 10; Length 110000;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 309
  Query Match 0.8%; Score 19; DB 10; Length 110000;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 310
  Query Match 0.8%; Score 19; DB 10; Length 110000;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 311
  Query Match 0.8%; Score 19; DB 10; Length 110000;
  Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 312
ID ABD32921 standard; DNA; 754086 BP.
DE Mouse cancer-associated genomic DNA MD19-002.
PN WO2004074320-A2.
PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 0.8%; Score 19; DB 13; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 313
ID ABD32923 standard; DNA; 788759 BP.
DE Human cancer-associated genomic DNA HD19-002.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 0.8%; Score 19; DB 13; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 314
ID AAX20249 standard; DNA; 116277 BP.
DE Borrelia burgdorferi polynucleotide sequence #2.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 0.8%; Score 19; DB 2; Length 116277;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 315
ID ADQ97301 standard; DNA; 127722 BP.
DE Human cancer associated sequence HD08-028, SEQ ID 278.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 0.8%; Score 19; DB 12; Length 127722;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 316
ID ADQ97651 standard; DNA; 127943 BP.
DE Human cancer associated sequence HD10-021, SEQ ID 628.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 0.8%; Score 19; DB 12; Length 127943;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 317
ID ABK49450 standard; DNA; 147309 BP.
DE Human transporter genomic DNA sequence.
Query Match 0.8%; Score 19; DB 6; Length 147309;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 318
ID ADR52892 standard; DNA; 151152 BP.
DE Drug therapy altered expressed gene #243.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 0.8%; Score 19; DB 13; Length 151152;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 319
ID ACF62730 standard; DNA; 164702 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:658.
PN WO2003013534-A2.

PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 0.8%; Score 19; DB 8; Length 164702;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 320
ID ADB20845 standard; DNA; 164702 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:658.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 0.8%; Score 19; DB 8; Length 164702;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 321
ID ADB87934 standard; DNA; 164702 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:658.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 0.8%; Score 19; DB 10; Length 164702;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 322
ID ADB96917 standard; DNA; 164702 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:658.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 0.8%; Score 19; DB 10; Length 164702;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 323
ID ADB92108 standard; DNA; 164702 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:658.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 0.8%; Score 19; DB 10; Length 164702;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 324
ID AAD58431 standard; DNA; 322101 BP.
DE Human PAOD1 genomic DNA.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 0.8%; Score 19; DB 10; Length 322101;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 325
ID ADI35046 standard; DNA; 322101 BP.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) genomic DNA sequence.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 0.8%; Score 19; DB 12; Length 322101;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 326
ID AAC58049 standard; DNA; 18 BP.
DE Human PRO1780 forward PCR primer SEQ ID NO:71.
PN WO200053750-A1.
PD 14-SEP-2000.

PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 327
ID AAF54529 standard; DNA; 18 BP.
DE Primer #136 used in the identification of proteins.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 328
ID ACD68568 standard; DNA; 18 BP.
DE Novel human secreted and transmembrane protein related primer #141.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 329
ID ACH04670 standard; DNA; 18 BP.
DE Human secreted/transmembrane protein PRO1780 Taqman PCR primer #1.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 330
ID ACD68214 standard; DNA; 18 BP.
DE Novel human secreted and transmembrane protein related primer #141.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 331
ID ADC18322 standard; DNA; 18 BP.
DE Human PRO PCR primer #138.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 332
ID ADD70968 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 333
ID ADD40045 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

```
  Query Match             0.8%;  Score 18;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
RESULT 334
ID   ADD70491 standard; DNA; 18 BP.
DE   Human PRO 1780 Taqman PCR primer #1.
PN   US2003054406-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.8%;  Score 18;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
RESULT 335
ID   ADD38612 standard; DNA; 18 BP.
DE   Human PRO 1780 Taqman PCR primer #1.
PN   US2003096955-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.8%;  Score 18;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
RESULT 336
ID   ADD39568 standard; DNA; 18 BP.
DE   Human PRO 1780 Taqman PCR primer #1.
PN   US2003096954-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.8%;  Score 18;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
RESULT 337
ID   ADD39091 standard; DNA; 18 BP.
DE   Human PRO 1780 Taqman PCR primer #1.
PN   US2003092061-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.8%;  Score 18;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
RESULT 338
ID   ADD40522 standard; DNA; 18 BP.
DE   Human PRO 1780 Taqman PCR primer #1.
PN   US2003082627-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.8%;  Score 18;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
RESULT 339
ID   ADE50743 standard; DNA; 18 BP.
DE   Human PRO 1780 Taqman PCR primer #1.
PN   US2003069179-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.8%;  Score 18;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
RESULT 340
ID   ADE20355 standard; DNA; 18 BP.
DE   Human PRO 1780 Taqman PCR primer #1.
PN   US2003092883-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             0.8%;  Score 18;  DB 10;  Length 18;
```

Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 341
ID ADE50266 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 342
ID ADE21824 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 343
ID ADF30249 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 344
ID ADF56142 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 345
ID ADH99646 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 346
ID ADE96826 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 347
ID ADF26137 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

RESULT 348
ID ADF25036 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.8%; Score 18; DB 12; Length 18;
  Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 349
ID ADF29772 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.8%; Score 18; DB 12; Length 18;
  Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 350
ID ADE97303 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.8%; Score 18; DB 12; Length 18;
  Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 351
ID ADH03341 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.8%; Score 18; DB 12; Length 18;
  Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 352
ID ADH04295 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.8%; Score 18; DB 12; Length 18;
  Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 353
ID ADH03818 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
  Query Match 0.8%; Score 18; DB 12; Length 18;
  Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 354
ID ADH04772 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
  Query Match 0.8%; Score 18; DB 12; Length 18;
  Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 355

ID ADH61773 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
  Query Match 0.8%; Score 18; DB 12; Length 18;
  Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 356
ID ADL94972 standard; DNA; 18 BP.
DE Human PRO 1780 Taqman PCR primer #1.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
  Query Match 0.8%; Score 18; DB 12; Length 18;
  Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 357
ID AAA96250 standard; DNA; 31 BP.
DE PCR primer for cDNA encoding a human Edg5 polypeptide.
PN WO200056135-A2.
PD 28-SEP-2000.
PA (REGC) UNIV CALIFORNIA.
  Query Match 0.8%; Score 18; DB 3; Length 31;
  Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 358
ID ADF99932 standard; cDNA; 90 BP.
DE Nicotiana tabacum variant bright yellow nucleotide sequence SEQ ID:448.
PN WO2003097790-A2.
PD 27-NOV-2003.
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
PA (VTTB-) VTT BIOTECHNOLOGY.
  Query Match 0.8%; Score 18; DB 12; Length 90;
  Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 359
ID ACD70068 standard; DNA; 100 BP.
DE E. coli K12 MG1655 biochip probe SEQ ID 1338.
PN EP1260592-A1.
PD 27-NOV-2002.
PA (MWGB-) MWG-BIOTECH AG.
  Query Match 0.8%; Score 18; DB 8; Length 100;
  Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 360
ID ACD70069 standard; DNA; 100 BP.
DE E. coli K12 MG1655 biochip probe SEQ ID 1339.
PN EP1260592-A1.
PD 27-NOV-2002.
PA (MWGB-) MWG-BIOTECH AG.
  Query Match 0.8%; Score 18; DB 8; Length 100;
  Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 361
ID ADO13357 standard; DNA; 113 BP.
DE SNP target #221 for single multiplex PCR detection method.
PN WO2004033649-A2.
PD 22-APR-2004.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
  Query Match 0.8%; Score 18; DB 12; Length 113;
  Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 362

ID AAF17410 standard; DNA; 220 BP.
DE K-DNA cleavage hotspot.
PN US6150160-A.
PD 21-NOV-2000.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UYPE-) UNIV PENNSYLVANIA.
  Query Match 0.8%; Score 18; DB 4; Length 220;
  Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 363
ID ADF12345 standard; DNA; 220 BP.
DE Human retrotransposon L1 EN substrate K-DNA.
PN US2003121063-A1.
PD 26-JUN-2003.
PA (UYPE-) UNIV PENNSYLVANIA.
  Query Match 0.8%; Score 18; DB 10; Length 220;
  Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 364
ID ADF58236 standard; cDNA; 240 BP.
DE Human polynucleotide sequence SEQ ID NO:603.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
  Query Match 0.8%; Score 18; DB 10; Length 240;
  Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 365
ID ADL85483 standard; DNA; 245 BP.
DE DNA up-regulated in murine common lymphoid myeloid cells SeqID 1876.
PN WO2003093445-A2.
PD 13-NOV-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
  Query Match 0.8%; Score 18; DB 12; Length 245;
  Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 366
ID ADL85482 standard; DNA; 245 BP.
DE DNA up-regulated in murine common lymphoid myeloid cells SeqID 1875.
PN WO2003093445-A2.
PD 13-NOV-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
  Query Match 0.8%; Score 18; DB 12; Length 245;
  Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 367
ID ACH88858 standard; DNA; 287 BP.
DE Human genome derived single exon probe #22053.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
  Query Match 0.8%; Score 18; DB 12; Length 287;
  Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 368
ID ADT96283 standard; cDNA; 295 BP.
DE Colon cancer associated human cDNA sequence #1790.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
  Query Match 0.8%; Score 18; DB 11; Length 295;

Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 369
ID AAZ32844 standard; DNA; 303 BP.
DE Human chemokine beta-R1 promoter.
PN US5977334-A.
PD 02-NOV-1999.
PA (CLEV-) CLEVELAND CLINIC FOUND.
Query Match 0.8%; Score 18; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 370
ID ABN84846 standard; DNA; 303 BP.
DE Human Beta R1 chemokine gene promoter.
PN US6414118-B1.
PD 02-JUL-2002.
PA (CLEV-) CLEVELAND CLINIC FOUND.
Query Match 0.8%; Score 18; DB 6; Length 303;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 371
ID AAS34210 standard; cDNA; 350 BP.
DE Human cDNA encoding a novel foetal antigen, SEQ ID No 734.
PN WO200155312-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 5; Length 350;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 372
ID ABQ85759 standard; DNA; 355 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 629.
PN US2002062014-A1.
PD 23-MAY-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 0.8%; Score 18; DB 6; Length 355;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 373
ID AAV87586 standard; cDNA; 361 BP.
DE EST clone DY656.
PN WO9845437-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.

Query Match 0.8%; Score 18; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 374
ID AAA44800 standard; cDNA; 365 BP.
DE Human secreted expressed sequence tag SEQ ID NO:1375.
PN WO200021991-A1.
PD 20-APR-2000.
PA (GEMY) GENETICS INST INC.
Query Match 0.8%; Score 18; DB 3; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 375
ID ADP66197 standard; cDNA; 365 BP.
DE Human cDNA from gene modulated by pro-inflammatory cytokines #17.
PN US2004110194-A1.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 0.8%; Score 18; DB 12; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 376
ID ABL79277 standard; cDNA; 399 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:2255.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 18; DB 6; Length 399;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 377
ID AAD15302 standard; cDNA; 402 BP.
DE Human PMS134 cDNA.
PN WO200161012-A1.
PD 23-AUG-2001.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
PA (KINZ/) KINZLER K.
PA (VOGE/) VOGELSTEIN B.
Query Match 0.8%; Score 18; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 378
ID ACH46946 standard; cDNA; 402 BP.
DE Human infant brain cDNA #1009.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 0.8%; Score 18; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;

RESULT 379
ID AAH76368 standard; cDNA; 426 BP.
DE Human PMS2-134 cDNA.
PN WO200159092-A2.
PD 16-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 0.8%; Score 18; DB 4; Length 426;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 380
ID AAH75045 standard; cDNA; 426 BP.
DE Nucleotide sequence of human mismatch repair protein PMS2-134.
PN WO200162945-A1.
PD 30-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (VOGE/) VOGELSTEIN B.
PA (KINZ/) KINZLER K W.
Query Match 0.8%; Score 18; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 381
ID ABK86092 standard; DNA; 426 BP.
DE Human cDNA encoding PMS2-134.
PN WO200238750-A1.
PD 16-MAY-2002.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 382
ID AAD39201 standard; cDNA; 426 BP.
DE Human mismatch repair protein, hPMS2-134 cDNA.
PN WO200237967-A1.
PD 16-MAY-2002.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 383
ID AAL48701 standard; DNA; 426 BP.
DE Human truncated mismatch repair protein PMS2-134 coding sequence.
PN WO200254856-A1.
PD 18-JUL-2002.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 384
ID AAD39773 standard; cDNA; 426 BP.
DE Human PMS2-134 cDNA.
PN WO200240499-A1.
PD 23-MAY-2002.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 385
ID ABX12943 standard; DNA; 426 BP.
DE DNA encoding human PMS2-134 protein.
PN WO2003012130-A1.
PD 13-FEB-2003.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 8; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 386
ID ACA89707 standard; cDNA; 426 BP.
DE cDNA encoding human PMS2-134 mismatch repair protein.

PN WO2003031937-A2.
PD 17-APR-2003.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 8; Length 426;
  Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 387
ID AAL57767 standard; cDNA; 426 BP.
DE Human mismatch repair protein PMS2-134 cDNA.
PN WO2003062435-A1.
PD 31-JUL-2003.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 9; Length 426;
  Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 388
ID ADA06251 standard; DNA; 426 BP.
DE DNA encoding the human mismatch repair, MMR, protein PMS2-134.
PN US2003068808-A1.
PD 10-APR-2003.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (KLIN/) KLINE J B.
  Query Match 0.8%; Score 18; DB 9; Length 426;
  Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 389
ID ADC89614 standard; cDNA; 426 BP.
DE Human PMS2-134 encoding cDNA SEQ ID NO:14.
PN WO2003072732-A2.
PD 04-SEP-2003.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 10; Length 426;
  Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 390
ID ADF17899 standard; DNA; 426 BP.
DE Human PMS2-134 cDNA, a mismatch repair gene.
PN US6576468-B1.
PD 10-JUN-2003.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 10; Length 426;
  Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 391
ID ADG62906 standard; cDNA; 426 BP.
DE Human dominant negative mismatch repair protein (PMS2-134) cDNA.
PN US2003165468-A1.
PD 04-SEP-2003.
PA (GRAS/) GRASSO L.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
  Query Match 0.8%; Score 18; DB 10; Length 426;
  Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 392
ID ADH62636 standard; cDNA; 426 BP.
DE Human mismatch repair protein PMS2-134 cDNA.
PN US2003143682-A1.
PD 31-JUL-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.

PA (SASS/) SASS P M.
Query Match 0.8%; Score 18; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 393
ID ADF78847 standard; cDNA; 426 BP.
DE Human dominant negative truncation hPMS2-134.
PN US2003186441-A1.
PD 02-OCT-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
Query Match 0.8%; Score 18; DB 12; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 394
ID ADG46774 standard; cDNA; 426 BP.
DE Human MMR protein (mismatch protein), PMS2-134 cDNA.
PN US2003091997-A1.
PD 15-MAY-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
Query Match 0.8%; Score 18; DB 12; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 395
ID ADO40073 standard; cDNA; 426 BP.
DE Human PMS2-134 mutant cDNA.
PN US6737268-B1.
PD 18-MAY-2004.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 12; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 396
ID ADP66683 standard; DNA; 426 BP.
DE Human mismatch repair protein PMS2-134 encoding DNA.
PN WO2004046330-A2.
PD 03-JUN-2004.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 12; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 397
ID ADR13890 standard; cDNA; 426 BP.
DE Human DNA mismatch repair protein PMS2-134 cDNA.
PN US2004158886-A1.
PD 12-AUG-2004.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 13; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 398
ID ACA43798 standard; DNA; 462 BP.
DE Prokaryotic essential gene #25455.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 0.8%; Score 18; DB 8; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 399
ID ADR29948 standard; cDNA; 475 BP.

DE Mouse gene trapped cDNA sequence, GTS #525.
PN US2004168209-A1.
PD 26-AUG-2004.
PA (ABUI/) ABUIN A.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
Query Match 0.8%; Score 18; DB 13; Length 475;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
RESULT 400
ID ACH50718 standard; cDNA; 501 BP.
DE Human mammary gland cDNA #123.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 0.8%; Score 18; DB 9; Length 501;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 401
ID ACH75158 standard; DNA; 507 BP.
DE Human genome derived single exon probe #8353.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 0.8%; Score 18; DB 12; Length 507;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 402
ID ADQ79683 standard; DNA; 507 BP.
DE Benzoate dioxygenase beta subunit (benB) DNA.
PN KR2003082683-A.
PD 23-OCT-2003.
PA (KIME/) KIM E S.
Query Match 0.8%; Score 18; DB 12; Length 507;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 403
ID AAH11550 standard; cDNA; 541 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:8385.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 0.8%; Score 18; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 404
ID ABV52391 standard; cDNA; 547 BP.
DE Human prostate expression marker cDNA 52382.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 0.8%; Score 18; DB 5; Length 547;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 405
ID ADQ56077 standard; DNA; 554 BP.
DE Novel canine microarray-related DNA sequence SeqID7379.

PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
  Query Match 0.8%; Score 18; DB 13; Length 554;
  Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 406
ID ABX78375 standard; cDNA; 585 BP.
DE Rice stress response protein EST #8.
PN US2002152497-A1.
PD 17-OCT-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.
PA (SAKA/) SAKAI H.
PA (WENG/) WENG Z.
  Query Match 0.8%; Score 18; DB 10; Length 585;
  Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 407
ID AAC10739 standard; cDNA; 587 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14814.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
  Query Match 0.8%; Score 18; DB 3; Length 587;
  Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 408
ID ABV55372 standard; cDNA; 590 BP.
DE Human prostate expression marker cDNA 55363.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match 0.8%; Score 18; DB 5; Length 590;
  Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 409
ID ADQ51591 standard; DNA; 609 BP.
DE Novel canine microarray-related DNA sequence SeqID2893.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
  Query Match 0.8%; Score 18; DB 13; Length 609;
  Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 410
ID AAA65944 standard; DNA; 636 BP.
DE E. coli proliferation associated coding sequence SEQ ID NO:136.
PN WO200044906-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.
  Query Match 0.8%; Score 18; DB 3; Length 636;
  Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 411
ID ABV55471 standard; cDNA; 637 BP.

DE Human prostate expression marker cDNA 55462.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 0.8%; Score 18; DB 5; Length 637;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 412
ID AAT29625 standard; cDNA to mRNA; 649 BP.
DE DNA mismatch repair protein coding sequence fragment PMS 5.
PN JP08107797-A.
PD 30-APR-1996.
PA (GANK-) ZH GAN KENKYUKAI.
PA (EISA) EISAI CO LTD.
Query Match 0.8%; Score 18; DB 2; Length 649;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 413
ID ABL67265 standard; DNA; 649 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5602.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 0.8%; Score 18; DB 6; Length 649;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 414
ID ACN92881 standard; DNA; 711 BP.
DE Breast cancer related marker, seq id 14031.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 0.8%; Score 18; DB 11; Length 711;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 415
ID ADK16796 standard; DNA; 738 BP.
DE Nanoarchaeum equitans cancer-associated (CA) gene #374.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 0.8%; Score 18; DB 12; Length 738;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 416
ID ADT48090 standard; cDNA; 750 BP.
DE Bacterial polynucleotide #22841.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 0.8%; Score 18; DB 13; Length 750;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 417
ID ACA27682 standard; DNA; 765 BP.
DE Prokaryotic essential gene #9339.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match 0.8%; Score 18; DB 8; Length 765;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

RESULT 418
ID ADE07742 standard; DNA; 777 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #808.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 18; DB 10; Length 777;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

RESULT 419
ID AAS63236 standard; cDNA; 780 BP.
DE Escherichia coli endonuclease III (Endo III) nth gene.
PN WO200173079-A2.
PD 04-OCT-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 0.8%; Score 18; DB 4; Length 780;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

RESULT 420
ID ADE07014 standard; DNA; 828 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #80.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 18; DB 10; Length 828;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

RESULT 421
ID AAK93666 standard; cDNA; 849 BP.
DE Human cDNA clone representative sequence, SEQ ID NO: 2126.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 0.8%; Score 18; DB 4; Length 849;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

RESULT 422
ID AAK92006 standard; cDNA; 849 BP.
DE Human cDNA 5'-end sequence, SEQ ID NO: 466.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 0.8%; Score 18; DB 4; Length 849;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

RESULT 423
ID ADL28433 standard; cDNA; 849 BP.
DE 5' end of a human cDNA molecule SeqID 466.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 0.8%; Score 18; DB 12; Length 849;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

RESULT 424
ID ADL30093 standard; cDNA; 849 BP.
DE 3' end of a representative human cDNA cluster SeqID 2126.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 0.8%; Score 18; DB 12; Length 849;

  Best Local Similarity   100.0%; Pred. No. 7.5e+02;
RESULT 425
ID   AAS02360 standard; DNA; 870 BP.
DE   Neomycin phosphotransferase gene.
PN   WO200123541-A2.
PD   05-APR-2001.
PA   (ALEX-) ALEXION PHARM INC.
  Query Match   0.8%; Score 18; DB 4; Length 870;
  Best Local Similarity   100.0%; Pred. No. 7.5e+02;
RESULT 426
ID   AAS02357 standard; DNA; 872 BP.
DE   Promoterless neomycin phosphotransferase gene cassette.
PN   WO200123541-A2.
PD   05-APR-2001.
PA   (ALEX-) ALEXION PHARM INC.
  Query Match   0.8%; Score 18; DB 4; Length 872;
  Best Local Similarity   100.0%; Pred. No. 7.5e+02;
RESULT 427
ID   ADP79709 standard; DNA; 1023 BP.
DE   Cycloclasticus aromatic ring dioxygenase gene cluster gene #4.
PN   WO2004050875-A1.
PD   17-JUN-2004.
PA   (MARI-) MARINE BIOTECHNOLOGY INST CO LTD.
  Query Match   0.8%; Score 18; DB 13; Length 1023;
  Best Local Similarity   100.0%; Pred. No. 7.5e+02;
RESULT 428
ID   AAK87321 standard; DNA; 1283 BP.
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42133.
PN   WO200157182-A2.
PD   09-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match   0.8%; Score 18; DB 4; Length 1283;
  Best Local Similarity   100.0%; Pred. No. 7.6e+02;
RESULT 429
ID   ADT41893 standard; cDNA; 1284 BP.
DE   Bacterial polynucleotide #16644.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match   0.8%; Score 18; DB 13; Length 1284;
  Best Local Similarity   100.0%; Pred. No. 7.6e+02;
RESULT 430
ID   ACC60654 standard; DNA; 1302 BP.
DE   Gene sequence #SEQ ID 90.
PN   EP1258494-A1.
PD   20-NOV-2002.
PA   (CELL-) CELLZOME AG.
  Query Match   0.8%; Score 18; DB 10; Length 1302;
  Best Local Similarity   100.0%; Pred. No. 7.6e+02;
RESULT 431
ID   ADK64151 standard; DNA; 1302 BP.
DE   Disease treating protein complex-derived gene #1300.
PN   EP1338608-A2.

PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 0.8%; Score 18; DB 10; Length 1302;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 432
ID AAC53146 standard; DNA; 1331 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 73531.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 18; DB 3; Length 1331;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 433
ID AAS34787 standard; cDNA; 1422 BP.
DE cDNA encoding novel human neoplastic disease associated polypeptide #21.
PN WO200155163-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 4; Length 1422;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 434
ID ABK43162 standard; cDNA; 1422 BP.
DE cDNA encoding human DNA repair and processing protein, SEQ ID No 22.
PN WO200155305-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 4; Length 1422;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 435
ID ADC45945 standard; cDNA; 1422 BP.
DE Human neoplastic disease-associated gene 21 cDNA #1.
PN US2003082758-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 10; Length 1422;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 436
ID ADA68340 standard; DNA; 1443 BP.
DE Arabidopsis thaliana gene, SEQ ID 792.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 0.8%; Score 18; DB 8; Length 1443;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 437
ID ABQ73708 standard; cDNA; 1455 BP.
DE Human colon specific nucleic acid (CSNA) SEQ ID NO:14.
PN WO200248370-A2.
PD 20-JUN-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 0.8%; Score 18; DB 6; Length 1455;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 438
ID AAN30040 standard; DNA; 1480 BP.
DE Sequence encoding bovine leukocyte interferon (IFN) -alpha-2 on plasmid
DE subclone p678EcoRI 3.2 kb.
PN EP88622-A.
PD 14-SEP-1983.

PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 1; Length 1480;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 439
ID AAV08178 standard; DNA; 1480 BP.
DE Bovine interferon-alpha 2 DNA.
PN US5827694-A.
PD 27-OCT-1998.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 2; Length 1480;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 440
ID AAV68161 standard; DNA; 1480 BP.
DE Bovine interferon-alpha 2 DNA.
PN US5831023-A.
PD 03-NOV-1998.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 2; Length 1480;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 441
ID ABS53994 standard; cDNA; 1480 BP.
DE cDNA encoding bovine leukocyte interferon alpha 2 (BoIFN-alpha2).
PN US6432677-B1.
PD 13-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 6; Length 1480;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 442
ID AAS85584 standard; cDNA; 1488 BP.
DE DNA encoding novel human diagnostic protein #21388.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 18; DB 5; Length 1488;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 443
ID AAH67065 standard; DNA; 1494 BP.
DE C glutamicum coding sequence fragment SEQ ID NO: 2100.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 0.8%; Score 18; DB 5; Length 1494;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 444
ID ADK65960 standard; DNA; 1497 BP.
DE C glutamicum mutated sigA gene #1.
PN DE10162729-A1.
PD 03-JUL-2003.
PA (DEGS) DEGUSSA AG.
Query Match 0.8%; Score 18; DB 10; Length 1497;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 445
ID ADK65958 standard; DNA; 1497 BP.
DE C glutamicum wild-type sigA gene.
PN DE10162729-A1.
PD 03-JUL-2003.
PA (DEGS) DEGUSSA AG.

Query Match 0.8%; Score 18; DB 10; Length 1497;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 446
ID ABV24039 standard; cDNA; 1503 BP.
DE Human prostate expression marker cDNA 24030.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 0.8%; Score 18; DB 5; Length 1503;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 447
ID ABV29922 standard; cDNA; 1504 BP.
DE Human prostate expression marker cDNA 29913.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 0.8%; Score 18; DB 5; Length 1504;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 448
ID AAD45435 standard; cDNA; 1565 BP.
DE Human MLH3 mutant cDNA #2.
PN US6416984-B1.
PD 09-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 6; Length 1565;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 449
ID ADC91963 standard; DNA; 1602 BP.
DE E. faecium DNA sequence SEQ ID 1590.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 0.8%; Score 18; DB 10; Length 1602;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 450
ID ADQ23147 standard; DNA; 1623 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5967.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 0.8%; Score 18; DB 12; Length 1623;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 451
ID ADD13289 standard; DNA; 1624 BP.
DE C. glutamicum stability and folding associated DNA RXA03793.
PN WO2003040180-A2.
PD 15-MAY-2003.
PA (BADI) BASF AG.
Query Match 0.8%; Score 18; DB 10; Length 1624;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 452
ID AAI99791 standard; cDNA; 1626 BP.
DE Human eukaryotic acetyl transferase 10 encoding cDNA.
PN WO200175026-A2.
PD 11-OCT-2001.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match 0.8%; Score 18; DB 6; Length 1626;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 453
ID ADQ25162 standard; DNA; 1634 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7982.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 0.8%; Score 18; DB 12; Length 1634;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 454
ID AAV34296 standard; DNA; 1688 BP.
DE Human secreted protein gene 11 clone HLTBS22.
PN WO9840483-A2.
PD 17-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 2; Length 1688;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 455
ID AAD44646 standard; cDNA; 1688 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HLTBS22, SEQ ID NO:21.
PN US2002077287-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
Query Match 0.8%; Score 18; DB 6; Length 1688;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 456
ID AAD44864 standard; cDNA; 1688 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HLTBS22, SEQ ID NO:21.
PN US2002076756-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.

Query Match 0.8%; Score 18; DB 6; Length 1688;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 457
ID ABX96976 standard; cDNA; 1688 BP.
DE Human secreted protein gene 11, cDNA.
PN US2002172994-A1.
PD 21-NOV-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.

Query Match 0.8%; Score 18; DB 8; Length 1688;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 458
ID ADG89748 standard; cDNA; 1688 BP.
DE Human cDNA from secreted protein gene 11.
PN US2003225009-A1.
PD 04-DEC-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.

Query Match 0.8%; Score 18; DB 12; Length 1688;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 459
ID ABZ24411 standard; cDNA; 1692 BP.
DE Human TBC1D1 nucleic acid 18558614.
PN WO200299049-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.

Query Match 0.8%; Score 18; DB 8; Length 1692;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 460
ID AAF15885 standard; cDNA; 1756 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:320.
PN WO200055174-A1.

PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 0.8%; Score 18; DB 3; Length 1756;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 461
ID ACN39313 standard; cDNA; 1764 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325551, SEQ ID NO:3378.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 0.8%; Score 18; DB 13; Length 1764;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 462
ID AAC46205 standard; DNA; 1767 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49283.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 18; DB 3; Length 1767;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 463
ID AAH76370 standard; cDNA; 1785 BP.
DE Human PMSR3 cDNA.
PN WO200159092-A2.
PD 16-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 0.8%; Score 18; DB 4; Length 1785;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 464
ID AAH75047 standard; cDNA; 1785 BP.
DE Nucleotide sequence of human mismatch repair protein PMSR3.
PN WO200162945-A1.
PD 30-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (VOGE/) VOGELSTEIN B.
PA (KINZ/) KINZLER K W.
Query Match 0.8%; Score 18; DB 5; Length 1785;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 465
ID ABX12946 standard; DNA; 1785 BP.
DE DNA encoding human PMSR3 protein.
PN WO2003012130-A1.
PD 13-FEB-2003.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 8; Length 1785;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 466
ID ACA89710 standard; cDNA; 1785 BP.
DE cDNA encoding human PMSR3 mismatch repair protein.
PN WO2003031937-A2.
PD 17-APR-2003.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 8; Length 1785;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 467
ID   AAL57773 standard; cDNA; 1785 BP.
DE   Human mismatch repair protein PMSR3 cDNA.
PN   WO2003062435-A1.
PD   31-JUL-2003.
PA   (MORP-) MORPHOTEK INC.
  Query Match   0.8%; Score 18; DB 9; Length 1785;
  Best Local Similarity   100.0%; Pred. No. 7.7e+02;
RESULT 468
ID   ADA06257 standard; DNA; 1785 BP.
DE   DNA encoding the human mismatch repair, MMR, protein PMSR3.
PN   US2003068808-A1.
PD   10-APR-2003.
PA   (NICO/) NICOLAIDES N C.
PA   (SASS/) SASS P M.
PA   (GRAS/) GRASSO L.
PA   (KLIN/) KLINE J B.
  Query Match   0.8%; Score 18; DB 9; Length 1785;
  Best Local Similarity   100.0%; Pred. No. 7.7e+02;
RESULT 469
ID   ADG62897 standard; cDNA; 1785 BP.
DE   Human PMSR3 cDNA.
PN   US2003165468-A1.
PD   04-SEP-2003.
PA   (GRAS/) GRASSO L.
PA   (NICO/) NICOLAIDES N C.
PA   (SASS/) SASS P M.
  Query Match   0.8%; Score 18; DB 10; Length 1785;
  Best Local Similarity   100.0%; Pred. No. 7.7e+02;
RESULT 470
ID   ADP66687 standard; DNA; 1785 BP.
DE   Human mismatch repair protein PMSR3 encoding DNA.
PN   WO2004046330-A2.
PD   03-JUN-2004.
PA   (MORP-) MORPHOTEK INC.
  Query Match   0.8%; Score 18; DB 12; Length 1785;
  Best Local Similarity   100.0%; Pred. No. 7.7e+02;
RESULT 471
ID   AAV04064 standard; cDNA; 1817 BP.
DE   Human RNA-binding protein ZPR1 cDNA.
PN   WO9746684-A1.
PD   11-DEC-1997.
PA   (UYMA-) UNIV MASSACHUSETTS.
  Query Match   0.8%; Score 18; DB 2; Length 1817;
  Best Local Similarity   100.0%; Pred. No. 7.7e+02;
RESULT 472
ID   ADR25106 standard; DNA; 1817 BP.
DE   Breast cancer prognosis marker #967.
PN   WO2004065545-A2.
PD   05-AUG-2004.
PA   (ROSE-) ROSETTA INPHARMATICS LLC.
PA   (NECA-) NETHERLANDS CANCER INST.
  Query Match   0.8%; Score 18; DB 13; Length 1817;
  Best Local Similarity   100.0%; Pred. No. 7.7e+02;
RESULT 473
ID   ADT44238 standard; cDNA; 1826 BP.
DE   Bacterial polynucleotide #18989.

PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 0.8%; Score 18; DB 13; Length 1826;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 474
ID ADQ79682 standard; DNA; 1853 BP.
DE Benzoate catabolic enzyme gene cluster #2.
PN KR2003082683-A.
PD 23-OCT-2003.
PA (KIME/) KIM E S.
Query Match 0.8%; Score 18; DB 12; Length 1853;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 475
ID ABX78376 standard; cDNA; 1861 BP.
DE Rice stress response protein EST #9.
PN US2002152497-A1.
PD 17-OCT-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.
PA (SAKA/) SAKAI H.
PA (WENG/) WENG Z.
Query Match 0.8%; Score 18; DB 10; Length 1861;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 476
ID ADK65962 standard; DNA; 1892 BP.
DE C glutamicum mutated sigA gene #2.
PN DE10162729-A1.
PD 03-JUL-2003.
PA (DEGS) DEGUSSA AG.
Query Match 0.8%; Score 18; DB 10; Length 1892;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 477
ID AAS75603 standard; cDNA; 1911 BP.
DE DNA encoding novel human diagnostic protein #11407.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 18; DB 5; Length 1911;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 478
ID ABK40202 standard; cDNA; 1920 BP.
DE Human G protein-coupled receptor (GPCR) 8 cDNA.
PN WO200202637-A2.
PD 10-JAN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 18; DB 6; Length 1920;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 479
ID ADS59106 standard; cDNA; 1935 BP.
DE Bacterial polynucleotide #11093.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
  Query Match 0.8%; Score 18; DB 13; Length 1935;
  Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 480
ID ABQ72684 standard; cDNA; 1980 BP.
DE Human MDDT encoding cDNA SEQ ID NO 236.
PN WO200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match 0.8%; Score 18; DB 6; Length 1980;
  Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 481
ID ABL90639 standard; cDNA; 1997 BP.
DE Human polynucleotide SEQ ID NO 1201.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 18; DB 6; Length 1997;
  Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 482
ID ACC61223 standard; DNA; 2000 BP.
DE Gene sequence #SEQ ID 1228.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
  Query Match 0.8%; Score 18; DB 10; Length 2000;
  Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 483
ID ADK63215 standard; DNA; 2000 BP.
DE Disease treating protein complex-derived gene #733.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
  Query Match 0.8%; Score 18; DB 10; Length 2000;
  Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 484
ID AAS87283 standard; cDNA; 2047 BP.
DE DNA encoding novel human diagnostic protein #23087.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 0.8%; Score 18; DB 5; Length 2047;
  Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 485
ID ABT31747 standard; DNA; 2152 BP.
DE GAAP-1 related DNA sequence #1.
PN WO200298916-A2.
PD 12-DEC-2002.

PA (CNRS) CENT NAT RECH SCI.
Query Match 0.8%; Score 18; DB 8; Length 2152;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 486
ID ABT31749 standard; DNA; 2178 BP.
DE GAAP-1 related DNA sequence #3.
PN WO200298916-A2.
PD 12-DEC-2002.
PA (CNRS) CENT NAT RECH SCI.
Query Match 0.8%; Score 18; DB 8; Length 2178;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 487
ID ACC46342 standard; cDNA; 2179 BP.
DE Human dithp zinc finger transcriptional regulator-encoding cDNA.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 0.8%; Score 18; DB 8; Length 2179;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 488
ID ADE31311 standard; DNA; 2179 BP.
DE Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 66.
PN WO2003062376-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 0.8%; Score 18; DB 10; Length 2179;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 489
ID ADB62959 standard; cDNA; 2228 BP.
DE Human cDNA encoding clone PROST20007170.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 0.8%; Score 18; DB 10; Length 2228;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 490
ID AAH16583 standard; cDNA; 2338 BP.
DE Human cDNA sequence SEQ ID NO:15667.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 0.8%; Score 18; DB 4; Length 2338;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 491
ID AAH18401 standard; cDNA; 2362 BP.
DE Human cDNA sequence SEQ ID NO:18465.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 0.8%; Score 18; DB 4; Length 2362;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 492
ID AAS81549 standard; cDNA; 2418 BP.
DE DNA encoding novel human diagnostic protein #17353.
PN WO200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 18; DB 5; Length 2418;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 493
ID AAH16233 standard; cDNA; 2492 BP.
DE Human cDNA sequence SEQ ID NO:15059.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 0.8%; Score 18; DB 4; Length 2492;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 494
ID ADA84026 standard; DNA; 2492 BP.
DE Human POM94 gene.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match 0.8%; Score 18; DB 8; Length 2492;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 495
ID ADB53889 standard; DNA; 2497 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4431.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 0.8%; Score 18; DB 10; Length 2497;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 496
ID ABL09142 standard; cDNA; 2498 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21908.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 0.8%; Score 18; DB 4; Length 2498;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 497
ID ABZ24410 standard; cDNA; 2576 BP.
DE Human TBC1D1 nucleic acid 5689552.
PN WO200299049-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 0.8%; Score 18; DB 8; Length 2576;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 498
ID ADR24190 standard; DNA; 2576 BP.
DE Breast cancer prognosis marker #51.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 0.8%; Score 18; DB 13; Length 2576;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 499
ID AAD15300 standard; cDNA; 2589 BP.
DE Human PMS2 cDNA.
PN WO200161012-A1.
PD 23-AUG-2001.

PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
PA (KINZ/) KINZLER K.
PA (VOGE/) VOGELSTEIN B.
Query Match 0.8%; Score 18; DB 4; Length 2589;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 500
ID AAQ90940 standard; DNA; 2687 BP.
DE Human wild type PMS1 gene, a MutL homologue.
PN WO9516793-A1.
PD 22-JUN-1995.
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 0.8%; Score 18; DB 2; Length 2687;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 501
ID AAQ14790 standard; cDNA; 2745 BP.
DE Haemonchus contortus phosphofructokinase gene.
PN WO9117260-A.
PD 14-NOV-1991.
PA (UPJO) UPJOHN CO.
Query Match 0.8%; Score 18; DB 2; Length 2745;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 502
ID AAQ97527 standard; cDNA; 2771 BP.
DE Human DNA repair protein hMLH3 coding sequence.
PN WO9520678-A1.
PD 03-AUG-1995.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 2; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 503
ID AAZ59955 standard; cDNA; 2771 BP.
DE cDNA encoding wild-type human mismatch repair enzyme PMS2.
PN CA2240609-A1.
PD 14-OCT-1999.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 0.8%; Score 18; DB 3; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 504
ID AAZ59956 standard; cDNA; 2771 BP.
DE cDNA encoding dominant negative PMS2 allele hPMS2-134.
PN CA2240609-A1.
PD 14-OCT-1999.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 0.8%; Score 18; DB 3; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 505
ID AAH76364 standard; cDNA; 2771 BP.
DE Human PMS2 cDNA.
PN WO200159092-A2.
PD 16-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 0.8%; Score 18; DB 4; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 506

ID AAH75041 standard; cDNA; 2771 BP.
DE Nucleotide sequence of human mismatch repair protein PMS2.
PN WO200162945-A1.
PD 30-AUG-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (VOGE/) VOGELSTEIN B.
PA (KINZ/) KINZLER K W.
  Query Match 0.8%; Score 18; DB 5; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 507
ID ABK86088 standard; DNA; 2771 BP.
DE Human cDNA encoding post meiotic segregation increased, PMS2.
PN WO200238750-A1.
PD 16-MAY-2002.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 6; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 508
ID AAD39197 standard; cDNA; 2771 BP.
DE Human mismatch repair protein, PMS2 cDNA.
PN WO200237967-A1.
PD 16-MAY-2002.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 6; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 509
ID AAL48697 standard; DNA; 2771 BP.
DE Human mismatch repair protein PMS2 coding sequence.
PN WO200254856-A1.
PD 18-JUL-2002.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 6; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 510
ID AAD45355 standard; cDNA; 2771 BP.
DE Human MLH3 cDNA.
PN US6416984-B1.
PD 09-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 18; DB 6; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 511
ID AAD45434 standard; cDNA; 2771 BP.
DE Human MLH3 mutant cDNA #1.
PN US6416984-B1.
PD 09-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 18; DB 6; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 512
ID AAD39769 standard; cDNA; 2771 BP.
DE Human PMS2 cDNA.
PN WO200240499-A1.
PD 23-MAY-2002.

PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 6; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 513
ID ABX12939 standard; DNA; 2771 BP.
DE DNA encoding human PMS2 protein.
PN WO2003012130-A1.
PD 13-FEB-2003.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 8; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 514
ID ACA89703 standard; cDNA; 2771 BP.
DE cDNA encoding human PMS2 mismatch repair protein.
PN WO2003031937-A2.
PD 17-APR-2003.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 8; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 515
ID ACD13763 standard; cDNA; 2771 BP.
DE Human MutL homologue, hMLH3, cDNA.
PN US2003027177-A1.
PD 06-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 9; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 516
ID AAL57763 standard; cDNA; 2771 BP.
DE Human mismatch repair protein PMS (post meiotic segregation) 2 cDNA.
PN WO2003062435-A1.
PD 31-JUL-2003.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 9; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 517
ID ADA06243 standard; DNA; 2771 BP.
DE DNA encoding the human mismatch repair, MMR, protein PMS2.
PN US2003068808-A1.
PD 10-APR-2003.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (KLIN/) KLINE J B.
Query Match 0.8%; Score 18; DB 9; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 518
ID ADC89606 standard; cDNA; 2771 BP.
DE Human PMS2 encoding cDNA SEQ ID NO:5.
PN WO2003072732-A2.
PD 04-SEP-2003.
PA (MORP-) MORPHOTEK INC.
Query Match 0.8%; Score 18; DB 10; Length 2771;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 519
ID ADF17891 standard; DNA; 2771 BP.
DE Human PMS2 cDNA, a mismatch repair gene.

PN US6576468-B1.
PD 10-JUN-2003.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 10; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 520
ID ADG62891 standard; cDNA; 2771 BP.
DE Human PMS2 cDNA.
PN US2003165468-A1.
PD 04-SEP-2003.
PA (GRAS/) GRASSO L.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
  Query Match 0.8%; Score 18; DB 10; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 521
ID ADH62628 standard; cDNA; 2771 BP.
DE Human mismatch repair protein PMS2 cDNA.
PN US2003143682-A1.
PD 31-JUL-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
  Query Match 0.8%; Score 18; DB 10; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 522
ID ADH60984 standard; cDNA; 2771 BP.
DE Human cDNA encoding mismatch repair protein hMLH3.
PN US6610477-B1.
PD 26-AUG-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYJO) UNIV JOHNS HOPKINS.
  Query Match 0.8%; Score 18; DB 10; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 523
ID ADF78839 standard; cDNA; 2771 BP.
DE Human mismatch repair protein PMS2.
PN US2003186441-A1.
PD 02-OCT-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
  Query Match 0.8%; Score 18; DB 12; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 524
ID ADG46766 standard; cDNA; 2771 BP.
DE Human MMR protein (mismatch protein), PMS2 cDNA.
PN US2003091997-A1.
PD 15-MAY-2003.
PA (NICO/) NICOLAIDES N C.
PA (GRAS/) GRASSO L.
PA (SASS/) SASS P M.
  Query Match 0.8%; Score 18; DB 12; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 525
ID ADO40065 standard; cDNA; 2771 BP.
DE Human PMS2 cDNA.

PN US6737268-B1.
PD 18-MAY-2004.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 12; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 526
ID ADP12816 standard; DNA; 2771 BP.
DE Reference mRNA sequence #30.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
  Query Match 0.8%; Score 18; DB 12; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 527
ID ADP66681 standard; DNA; 2771 BP.
DE Human mismatch repair protein PMS2 encoding DNA.
PN WO2004046330-A2.
PD 03-JUN-2004.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 12; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 528
ID ADQ87551 standard; cDNA; 2771 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4429.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
  Query Match 0.8%; Score 18; DB 12; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 529
ID ADQ87314 standard; cDNA; 2771 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4191.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
  Query Match 0.8%; Score 18; DB 13; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 530
ID ADR13882 standard; cDNA; 2771 BP.
DE Human DNA mismatch repair protein PMS2 cDNA.
PN US2004158886-A1.
PD 12-AUG-2004.
PA (MORP-) MORPHOTEK INC.
  Query Match 0.8%; Score 18; DB 13; Length 2771;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 531
ID ACN41774 standard; cDNA; 2787 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:649.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
  Query Match 0.8%; Score 18; DB 13; Length 2787;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 532
ID ADR07917 standard; cDNA; 2890 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1423.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match 0.8%; Score 18; DB 13; Length 2890;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 533
ID ABQ55018 standard; cDNA; 2897 BP.
DE Human ovarian antigen HTGFW12 cDNA, SEQ ID NO:898.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 0.8%; Score 18; DB 6; Length 2897;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 534
ID ADR07498 standard; cDNA; 2988 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1004.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match 0.8%; Score 18; DB 13; Length 2988;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 535
ID AAK94796 standard; cDNA; 2989 BP.
DE Human full-length cDNA, SEQ ID NO: 3914.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
  Query Match 0.8%; Score 18; DB 4; Length 2989;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 536
ID ADL31881 standard; cDNA; 2989 BP.
DE Full length human cDNA clone SeqID 3914.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match 0.8%; Score 18; DB 12; Length 2989;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 537
ID AAS81539 standard; cDNA; 3006 BP.
DE DNA encoding novel human diagnostic protein #17343.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 0.8%; Score 18; DB 5; Length 3006;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 538
ID ABZ24412 standard; cDNA; 3023 BP.
DE Human TBC1D1 nucleic acid 17939551.
PN WO200299049-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
  Query Match 0.8%; Score 18; DB 8; Length 3023;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 539

ID ABL23724 standard; DNA; 3137 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 22645.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
  Query Match 0.8%; Score 18; DB 4; Length 3137;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 540
ID ADL14038 standard; cDNA; 3258 BP.
DE Human cDNA encoding sarcoma-associated antigen NY-SAR-5.
PN US2004063101-A1.
PD 01-APR-2004.
PA (SCAN/) SCANLAN M J.
PA (LEES/) LEE S.
PA (OLDL/) OLD L J.
  Query Match 0.8%; Score 18; DB 12; Length 3258;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 541
ID AAI59640 standard; cDNA; 3281 BP.
DE Human polynucleotide SEQ ID NO 3629.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 0.8%; Score 18; DB 4; Length 3281;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 542
ID ABX05239 standard; cDNA; 3317 BP.
DE Human novel polynucleotide #254.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
  Query Match 0.8%; Score 18; DB 8; Length 3317;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 543
ID AAI57854 standard; cDNA; 3326 BP.
DE Human polynucleotide SEQ ID NO 57.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 0.8%; Score 18; DB 4; Length 3326;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 544
ID ADB80378 standard; DNA; 3332 BP.
DE Human MDDT gene SEQ ID NO:65.
PN WO2003016497-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match 0.8%; Score 18; DB 9; Length 3332;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 545
ID ADQ18716 standard; DNA; 3367 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1535.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
  Query Match 0.8%; Score 18; DB 12; Length 3367;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 546
ID ABT42727 standard; DNA; 3381 BP.
DE Human neuroblastoma-related DNA sequence, SEQ ID NO:8.
PN WO2002103017-A1.
PD 27-DEC-2002.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
  Query Match 0.8%; Score 18; DB 8; Length 3381;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 547
ID ABV29011 standard; cDNA; 3382 BP.
DE Human prostate expression marker cDNA 29002.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match 0.8%; Score 18; DB 5; Length 3382;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 548
ID ABV23171 standard; cDNA; 3382 BP.
DE Human prostate expression marker cDNA 23162.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match 0.8%; Score 18; DB 5; Length 3382;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 549
ID AAZ27622 standard; DNA; 3496 BP.
DE Plasmid TOPI-1.
PN WO9949063-A1.
PD 30-SEP-1999.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
  Query Match 0.8%; Score 18; DB 2; Length 3496;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 550
ID ADM47670 standard; DNA; 3501 BP.
DE Polynucleotide sequence #88 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
  Query Match 0.8%; Score 18; DB 12; Length 3501;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 551
ID ADM18411 standard; DNA; 3512 BP.
DE Human chromosome 1ptel subtelomeric DNA probe SEQ ID NO:35.
PN WO2004029283-A2.
PD 08-APR-2004.
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
  Query Match 0.8%; Score 18; DB 12; Length 3512;
  Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 552
ID ACC46686 standard; cDNA; 3607 BP.
DE Human dithp biochemical pathway protein-encoding cDNA.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 0.8%; Score 18; DB 8; Length 3607;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 553
ID ADE57649 standard; DNA; 3640 BP.
DE Human gene J00265, SEQ ID NO 3511.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 0.8%; Score 18; DB 10; Length 3640;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 554
ID ADA70734 standard; DNA; 3645 BP.
DE Rice gene, SEQ ID 4057.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 0.8%; Score 18; DB 8; Length 3645;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 555
ID ADQ64879 standard; cDNA; 3646 BP.
DE Novel human cDNA sequence #2040.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 0.8%; Score 18; DB 12; Length 3646;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 556
ID ADI57183 standard; cDNA; 3663 BP.
DE Human PLC-beta1 encoding cDNA SEQ ID NO:3.
PN WO2004007754-A2.
PD 22-JAN-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 0.8%; Score 18; DB 12; Length 3663;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 557
ID ABA96004 standard; cDNA; 3700 BP.
DE Human lipid metabolism enzyme-4 (LME-4) cDNA.
PN WO200185956-A2.
PD 15-NOV-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 0.8%; Score 18; DB 6; Length 3700;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 558
ID AAC77404 standard; cDNA; 3727 BP.
DE Human ORFX ORF2959 polynucleotide sequence SEQ ID NO:5917.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 18; DB 3; Length 3727;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 559
ID ADJ80212 standard; cDNA; 3737 BP.
DE Novel human nucleic acid-associated protein coding sequence #30.
PN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 0.8%; Score 18; DB 10; Length 3737;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 560
ID ABL90217 standard; cDNA; 3751 BP.
DE Human polynucleotide SEQ ID NO 779.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 18; DB 6; Length 3751;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 561
ID AAZ27621 standard; DNA; 3766 BP.
DE Plasmid TOP-1.
PN WO9949063-A1.
PD 30-SEP-1999.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 0.8%; Score 18; DB 2; Length 3766;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 562
ID ADS47565 standard; cDNA; 3822 BP.
DE Bacterial polynucleotide #2308.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 0.8%; Score 18; DB 13; Length 3822;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

RESULT 563
ID ABL14239 standard; cDNA; 3924 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37199.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 0.8%; Score 18; DB 4; Length 3924;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;

RESULT 564
ID AAZ50906 standard; cDNA; 3983 BP.
DE Human TBC-1 cDNA from first transcript.
PN WO200008209-A2.
PD 17-FEB-2000.
PA (GEST) GENSET.
Query Match 0.8%; Score 18; DB 3; Length 3983;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;

RESULT 565
ID ABZ24414 standard; cDNA; 3983 BP.
DE Human TBC1D1 1st transcript.
PN WO200299049-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 0.8%; Score 18; DB 8; Length 3983;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;

RESULT 566
ID AAZ50907 standard; cDNA; 3988 BP.
DE Human TBC-1 cDNA from second transcript.